

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 23:11:45 ; Search time 63.6 Seconds
(without alignments)
328.331 Million cell updates/sec

Title: US-09-679-705-24
Perfect score: 987
Sequence: 1 MSЛИНТКИРКФКНQAFKNGE AKWKEGEATLAPSILVKG 188
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

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4: /SIDS5/geodata/geneseq/geneseqp-embl/AA1983.DAT:*

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6: /SIDS5/geodata/geneseq/geneseqp-embl/AA1985.DAT:*

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8: /SIDS5/geodata/geneseq/geneseqp-embl/AA1987.DAT:*

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22: /SIDS5/geodata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	970.5	98.3	187 22	AAU31488 E. coli cellular p
2	963.5	97.6	187 22	AAU38121 Salmonella typhi c
3	644.5	65.3	189 22	AAU35922 Staphylococcus aur
4	644.5	65.3	189 22	AAU36016 Staphylococcus aur
5	644.5	65.3	189 22	AAU37159 Staphylococcus aur
6	644.5	65.3	189 22	AAU37549 Staphylococcus aur
7	626	63.4	186 20	AAW30015 Streptococcus muta
8	605.5	61.3	187 22	AAU36183 Pseudomonas aerugi
9	563.5	57.1	187 22	AAU34999 Enterococcus fae
10	546	55.3	145 22	AAU63080 Propionibacterium
11	497.5	50.4	1873 22	ABG14982 Novel human diagno

ALIGNMENTS

RESULT 1	RAU34488	ID RAU34488 standard; Protein; 187 AA.
	XX	AC AAU34488;
DT 14-FEB-2002 (first entry)	XX	DE E. coli cellular proliferation protein #69.
XX	XX	KW Antisense; prokaryotic cellular proliferation protein;
XX	XX	KW antibiotic; antibacterial; drug design.
OS Escherichia coli.	XX	
PN WO2001170925-A2.	XX	
PD 27-SEP-2001.	XX	
PP 21-MAR-2001; 2001WO-US09180.	XX	
PR 21-MAR-2000; 2000US-191078P.	PR	
PR 23-MAY-2000; 2000US-206848P.	PR	
PR 26-MAY-2000; 2000US-20772P.	PR	
PR 23-OCT-2000; 2000US-242578P.	PR	
PR 27-NOV-2000; 2000US-253625P.	PR	
PR 22-DEC-2000; 2000US-257931P.	PR	
PR 16-FEB-2001; 2001US-269308P.	PR	
PA (ELIT-) ELITRA PHARM INC.	PA	
XX Hessebeck R., Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;	PI Yamamoto RT, Xu HH;	
XX	XX	

DE Staphylococcus aureus cellular proliferation protein #98.
 XX
 KW Antisense; prokaryotic cellular proliferation protein;
 KW antisense; antibacterial; drug design

Antisense: prokaryotic cellular proliferation protein antibiotic: antibacterial drug design

QY	179	APSLDLVGKI	188
Db	180	qpgldlvgki	189

Db 180 qpgldlvkgi 189

Staphylococcus aureus.
WO200170955-A2.

RESULT 4
AAU36816 ID AAU36816 standard; Protein: 189 AA..
XX

21-MAR-2001; 2001WO-US09180.

DT
XX
DE
YY
Staphylococcus aureus cellular proliferation protein #986..

26-MAY-2000; 2000US-20/2/P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.

OS OS
XX KW KW
Staphylococcus aureus.

(ELIT-) ELITRA PHARM INC.

PN WO200170955-A2.
XX
PD 27-SEP-2001.
YY

YAMAMOTO RT; XU HT; WPI: 2001-611495/70.
N-FSDB; RASS51681.

New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -

	PP	XX	21-MAR-2001; 2001WO-US09180
PR	21-MAR-2000;	2000US-191078P	
PR	23-MAY-2000;	2000US-206648P	
PR	26-MAY-2000;	2000US-207727P	
PR	23-OCT-2000;	2000US-245725P	
PR	27-NOV-2000;	2000US-253252P	

Example 3 ; Seq ID NO 5318; 511pp; English.
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the

PR 22-DEC-2000; 20000US-25/931P.
PR 16-FEB-2001; 2001US-26930BP.
XX
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XX

genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, to identify proteins used in proliferation, to express these proteins,

and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen

PT antibiotics, comprise sequences of antisense nucleic acids -
Example 3: Seq ID No 12409; 511p; English.

Sequence 189 AA;

CC pneumoniae, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used

Query Match 65.3%; Score 644.5; DB 22; Length 189;
 Best Local Similarity 64.2%; Pred. NO. 2.1e-66;
 Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2

CC
CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation.

QY 1 MSLINTKIKPKNQAF--KNGEFIEITEKDEGRMSVFFFPADPTEVCPTELGVDVADH 58
 ||||| :||| ||| | :|| :|| :|| ||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1 mslinkeilpftaqadpkkdqfkevtqedikgsws-vcfypadisfvcpelteledlqnq 59
 QY 59 YEELQKGIVYAVASDTHFKAMHSSETIAKIKYAMGDPGALTRFDNMEDEGL 118
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 60 yeelqkgivnfvstadvthfkawhdhsaiskitytmqigdpsqtirfdvdaetgl 119
 QY 119 ADRAFVWVDDQGIQIAEVREGIGRDAASDLIRKIKAAQVASHGEVCAPKWSEATL 178
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 120 aqrgtfidpdgvqaseinadgigrdastlahkikaagyvrknpgcvcakweegaktl 179
 QY 179 APSDLIVGKI 188
 Db 180 qpgidivgki 189

RESULT 5

AC AAU37159;
 AC AAU37159; standard; Protein: 189 AA.

XX DT 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #1329.

XX KW Antisense; prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAR-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-20777P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX PA (ELIT-) ELTRA PHARM INC.

XX I Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 XX Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.
 DR N-PSDB; AAS55018.

XX PT New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids - Example 3; Seq ID No 12752; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ipo.int/pub/published_pct_sequences.

CC Sequence 189 AA;

Query Match 65.3%; Score 644.5; DB 22; Length 189; Best Local Similarity 64.2%; Pred. No. 2.1e-56; Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2; Index 40; Gapopen 40; Gapextend 1; Gapcost 1; Gapwidth 1; Gappen 1; Gapend 1; Gapindel 1; Gapopen2 1; Gapextend2 1; Gapcost2 1; Gapwidth2 1; Gappen2 1; Gapend2 1; Gapindel2 1; Gapopen3 1; Gapextend3 1; Gapcost3 1; Gapwidth3 1; Gappen3 1; Gapend3 1; Gapindel3 1; Gapopen4 1; Gapextend4 1; Gapcost4 1; Gapwidth4 1; Gappen4 1; Gapend4 1; Gapindel4 1; Gapopen5 1; Gapextend5 1; Gapcost5 1; Gapwidth5 1; Gappen5 1; Gapend5 1; Gapindel5 1; Gapopen6 1; Gapextend6 1; Gapcost6 1; Gapwidth6 1; Gappen6 1; Gapend6 1; Gapindel6 1; Gapopen7 1; Gapextend7 1; Gapcost7 1; Gapwidth7 1; Gappen7 1; Gapend7 1; Gapindel7 1; Gapopen8 1; Gapextend8 1; Gapcost8 1; Gapwidth8 1; Gappen8 1; Gapend8 1; Gapindel8 1; Gapopen9 1; Gapextend9 1; Gapcost9 1; Gapwidth9 1; Gappen9 1; Gapend9 1; Gapindel9 1; Gapopen10 1; Gapextend10 1; Gapcost10 1; Gapwidth10 1; Gappen10 1; Gapend10 1; Gapindel10 1; Gapopen11 1; Gapextend11 1; Gapcost11 1; Gapwidth11 1; 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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes themselves and the encoded proteins. The prokaryotes used are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic

format directly from WIPO at
ftp://wipo.int/pub/published_pct_sequences.

Sequence 139 AA:

	Query Match	Score	DB	Length
Best Local Similarity	64.3%	644.5	22	189
Matches	122;	Conservative	25;	Mismatches 40; Indels 3; Gaps 2;
QY	1	MSLINTKIKPPKNAF-KNGEEFEITEKDETEGRMSVFFPFYPADEFTFCVCPTELGDVADHE 58		
Db	1	mstinekkelpftqafqfpkqflevtedeklkswsr-vcfyfadfsfvctedlqng 59		
QY	59	YEELQKLGVDVAVSTDTHTHKAWHSSSETTAKIKYANIGDPTGALTRNFNRNREDEGL 118		
Db	60	yeeqklgvnfsystdthvhkawhdnsdaisktyunigdpsqtinmfdideatgl 119		
QY	119	ADRATFVWIDPQQLQIAIEVTAEGGRDASDLRIRKTAQYVASHPEGVCPKWKGEATLP 178		
Db	120	aqrgeffidpdgvvqaseinaddigrdastlankikaqyvrknpgcavcpakweegaktlp 179		
QY	179	APSDLVGKI 188		
Db	180	qpgidalvgki 189		

	Query Match	Score	DB	Length
Best Local Similarity	60.6%	626	20	186
Matches	114;	Conservative	29;	Mismatches 43; Indels 2; Gaps 2;
QY	1	MSLINTKIKPPKNAFKNNSERIETEKDETEGRMSVFFPFYPADEFTFCVCPTELGDVADHE 60		
Db	1	mstivkgemvnsfsaqhyqgeftvntndekqkwav-fcypadfsfvctedlqngya 59		
QY	61	ELQKLGVDVAVSTDTHTHKAWHSSSETTAKIKYANIGDPTGALTRNFNRNREDEGL 120		
Db	60	tlqlslgvnevyssvstdthvhkawhdnsdaisktyunigdpsqtinmfdideatgl 118		
QY	121	RATEFVWIDPQQLQIAIEVTEGIGRDASDLRIRKTAQYVASHPEGVCPKWKGEATLP 180		
Db	119	rgttfidpdgqjilqmmnevnaqgigrdastlirkvraaqyirqhpgcavcpakwkegaetlp 178		
QY	181	SLDLVGKI 188		
Db	179	slidvgki 186		

RESULT	8
ID	AAU36183
ID	AAU36183 standard; Protein; 186 AA.
XX	AAU6183;
AC	AAU6183;
XX	AAU6183;
DT	14-FEB-2002 (first entry)
XX	Pseudomonas aeruginosa cellular proliferation protein #173.
DE	Pseudomonas aeruginosa cellular proliferation protein #173.
XX	Antisense; prokaryotic cellular proliferation protein;
KW	antibiotic; antibacterial; drug design.
OS	Pseudomonas aeruginosa.
XX	WO200170955-A2.
PN	W0200170955-A2.
XX	27-SEP-2001.
PD	2001WO-US09180.
XX	21-MAR-2001; 2001WO-US09180.
PR	21-MAR-2000; 2000US-191078P.
PR	23-MAY-2000; 2000US-20648P.
PR	26-MAY-2000; 2000US-20727P.
PR	23-OCT-2000; 2000US-242278P.
PR	27-NOV-2000; 2000US-25325P.
PR	22-DEC-2000; 2000US-25731P.
PR	16-FEB-2001; 2001US-269308P.
XX	(ELIT-) ELTRA PHARM INC.
XX	Haselbeck R, Ohlsen KL, zyskind JW, Wall D, Trawick JD, Carr GJ;
PI	Yamamoto RT, Xu HH;
DR	WPI; 2001-611495/70.

XX DR
 XX PT
 XX PT New polynucleotides for the identification and development of
 XX antibiotics, comprise sequences of antisense nucleic acids -
 XX Example 3; Seq ID No 11776; 51PP; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 Note: The sequence data for this patent did not form part
 of the printed specification, but was obtained in electronic
 format directly from WIPO at
 ftp://wipo.int/pub/published_pct_sequences.
 XX
 SQ sequence 187 AA;
 Query Match 61.3%; Score 605.5; DB 22; Length 187;
 Best Local Similarity 58.5%; Pred. No. 6.9e-62; Indels 1; Gaps 1;
 Matches 110; Conservative 32; Mismatches 45; Indels 1; Gaps 1;
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 QY 1 MSLINTKIKPKRNQAFNGEIEITEKDTEGRWSVFFFYPADFTFVCPTELGDVADHYE 60
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 1 mslintqypfkvnawfhngkfleveesikglwsvlfm-paaftfncpteedaannq 59
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 QY 61 ELQKLGVDVVAVSTDTHTHKAWSSETIATKIKYAMGDPGTALTRNFNDNMREDEGLAD 120
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 Db 60 erqkagaevyyvttddhifskhwetsspgvqaqfpilgdpbtqlnafgvhipeeglal 119
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 QY 121 RATFVYDPOGIQIAEVTAEGTGRDASDLRKIKAAQYVASHGEVCAPAKWKGREATAP 180
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 120 rgtfvinepgviktvehsneiardvgetvrkikaqdytaantpbgevcakwkegektiapt 179
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 QY 181 SLDRVKI 188
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 AAU34998 standard; Protein; 187 AA.
 ID AAU34998;
 AC AAU34998;
 XX DT 14-FEB-2002 (first entry)
 DE Enterococcus faecalis cellular proliferation protein #285.
 KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 OS Enterococcus faecalis.
 XX PN WO200170955-A2.
 PD 27-SEP-2001.
 XX PF 21-MAR-2001; 2001WO-US09180.
 PR 21-MAR-2000; 2000US-191078P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX DR Haselbeck R., Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX DR N-PSDB; RAS52857.
 XX PR New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX PS Example 3; Seq ID No 10591; 51PP; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 Note: The sequence data for this patent did not form part
 of the printed specification, but was obtained in electronic
 format directly from WIPO at
 ftp://wipo.int/pub/published_pct_sequences.
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 SQ sequence 187 AA;
 Query Match 57.1%; Score 563.5; DB 22; Length 187;
 Best Local Similarity 54.3%; Pred. No. 5.2e-57; Indels 1; Gaps 1;
 Matches 102; Conservative 39; Mismatches 46; Indels 1; Gaps 1;
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 Db 60 hlgeincevysvedshyvhkawadatigkjkpmplapngqgarffgvldesasmay 119
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 QY 121 RATFVYDPOGIQIAEVTAEGTGRDASDLRKIKAAQYVASHGEVCAPAKWKGREATAP 180
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 QY 181 SLDRVKI 188
 Db 180 sdrlvkgki 187
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 AAU63080
 ID AAU63080 standard; Protein; 145 AA.
 AC AAU63080;
 XX DT 27-FEB-2002 (first entry)
 XX DE Propionibacterium acnes immunogenic protein #23976.
 DE

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PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138540.	PR	10-AUG-1999;	99US-0148171.	PR	10-AUG-1999;	99US-0148171.
PR	10-JUN-1999;	99US-0138847.	PR	11-AUG-1999;	99US-0148319.	PR	11-AUG-1999;	99US-0148319.
PR	14-JUN-1999;	99US-0139119.	PR	12-AUG-1999;	99US-0148341.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139452.	PR	13-AUG-1999;	99US-0148565.	PR	13-AUG-1999;	99US-0148565.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148684.	PR	13-AUG-1999;	99US-0148684.
PR	17-JUN-1999;	99US-0139492.	PR	16-AUG-1999;	99US-0149368.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139454.	PR	17-AUG-1999;	99US-0149175.	PR	17-AUG-1999;	99US-0149175.
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PR	18-JUN-1999;	99US-0139459.	PR	23-AUG-1999;	99US-0150080.	PR	23-AUG-1999;	99US-0150080.
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PR	21-JUN-1999;	99US-0139817.	PR	30-AUG-1999;	99US-0151303.	PR	30-AUG-1999;	99US-0151303.
PR	22-JUN-1999;	99US-0139899.	PR	31-AUG-1999;	99US-0151438.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140353.	PR	01-SEP-1999;	99US-0151930.	PR	01-SEP-1999;	99US-0151930.
PR	23-JUN-1999;	99US-0140354.	PR	07-SEP-1999;	99US-0152363.	PR	07-SEP-1999;	99US-0152363.
PR	24-JUN-1999;	99US-0140695.	PR	10-SEP-1999;	99US-0153070.	PR	10-SEP-1999;	99US-0153070.
PR	28-JUN-1999;	99US-0140833.	PR	13-SEP-1999;	99US-0153158.	PR	13-SEP-1999;	99US-0153158.
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XX Protein identification; signal transduction Pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX OS Arabidopsis thaliana.

XX DE Arabidopsis thaliana Protein Fragment SEQ ID NO: 57684.

XX KW Protein identification; signal transduction Pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX KW DE Arabidopsis thaliana Protein Fragment SEQ ID NO: 57684.

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Search completed: May 19, 2002, 01:14:12
 Job time: 7347 sec

RESULT 3
US-09-004-716-2

Sequence 2, Application US/09004/16
Patent No. 6031077

GENERAL INFORMATION:
APPLICANT: Klimowski, Laura
TITLE OF INVENTION: PARASITIC HELMINTH LARVAL THIOL SPECIFIC
TITLE OF INVENTION: ANTOXIDANT PROTEINS, NUCLEIC ACID MOLECULES, AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,716
FILING DATE: 2000-09-18

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,716
FILING DATE: 2000-09-18

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,262
FILING DATE: 2001-09-17

ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE DOCKET NUMBER: 2618-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
TOPeOLOGY: linear
MOLECULE TYPE: protein

US-09-004-716-2

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Sequence 15, Application US/08467265
Patent No. 5985612

GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gantz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-467-265-15

Query Match 34.9%; Score 344.5; DB 2; Length 198;
Best Local Similarity 38.7%; Pred. No. 1.7e-33; Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

Query 5 NTKI-KP--FKNQAKNGEIEIETEKDTGCRWSFFFFPADFFVCPELGVADHYE 60
Db 5 NARIKGAPDFKATAVDGAKFKEVKLSDYKGKY-VLLEFFPLDFFVCPELIAFSNRAB 63

Query 61 ELQKLGVDVVAVSTDTHFTKAWHSSET--IAKIKYAMIGDPGALTNRFDNNREDEGL 117
Db 64 DFRKGCVELGVQVSQFNHLAWNIDRKRMGGCGNNIPILADTNITISRAYGVLEDDGIALYRGLFIID 123

Query 118 LADRATFVDFOGIIQIAIEVTAEGIGRDASDLRKIKAAQYVASHGEVCPAKWKEGETLAPSL 177
Db 124 IAYRGFLIDGKGVRQITNDLPVGRSVDETLRLIQAFQFDNH-GEVCPANWQPGSEAIKPGV 182

Query 178 LAPSLD 183
Db 183 IKPNVD 188

RESULT 4
US-08-467-265-15
Sequence 15, Application US/08467265
Patent No. 5985612

GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang

Gentz, Reiner
 Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-Jun-1995
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 PRACTICE NUMBER: 325800-456
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
 LENGTH: 198 amino acids
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-08-467-265-15

Query Match Similarity 34.9%; Score 344.5; DB 4; Length 198;
 Best Local Similarity 38.7%; Pred. No. 1.7e-33;
 Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

Qy 5 NTKI-KP--FKNQAFKNGEFILETEKDTEGRWSVFFFYPADTFVCPTELGODAVDHYE 60
 | :| || | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 5 NARIGKPAFDKATAVWDGAFKEVLSKDSLKGKY-WLFLFPDLDFVCPEITAFSNRAE 63

Qy 61 ELQKLGVDYAVSSTDTHFKAWHSSET--IAKIKYAMIGDTGALTRNFDDNNREDEG 117
 | :| || | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| |
 Db 64 DFRKLGCVEVGSVSDOFNHLAWINPRKEGGGLGPLNLNPILGDVYRLSDGYVLTDEG 123

Qy 118 LADRATFVWPGQIQAIEVTAEGIGRDAASDLRKIKAQYVASHPGEVCPAKNKEGEAT 177
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 Db 124 IAYRGLFLIDGKGVLRQITYVNDLPVGRSVDREALRLVQAFQTDEH-GEVCPAGWKPGSDT 182

Qy 178 LAPSLD 183
 | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 183 IKPNVD 188

RESULT 5
 US-08-467-265-16
 ; Sequence 16, Application US/08467265
 ; Patent No. 5985612

GENERAL INFORMATION:

APPLICANT: Ni, Jian
 APPLICANT: YU, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey

ADDRESSEE: STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/407,891
 FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 PRACTICE NUMBER: 325800-456
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
 LENGTH: 198 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-407-891-15

Query Match Similarity 34.9%; Score 344.5; DB 4; Length 198;
 Best Local Similarity 38.7%; Pred. No. 1.7e-33;
 Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

Qy 5 NTKI-KP--FKNQAFKNGEFILETEKDTEGRWSVFFFYPADTFVCPTELGODAVDHYE 60
 | :| || | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 5 NARIGKPAFDKATAVWDGAFKEVLSKDSLKGKY-WLFLFPDLDFVCPEITAFSNRAE 63

Qy 61 ELQKLGVDYAVSSTDTHFKAWHSSET--IAKIKYAMIGDTGALTRNFDDNNREDEG 117
 | :| || | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| |
 Db 64 DFRKLGCVEVGSVSDOFNHLAWINPRKEGGGLGPLNLNPILGDVYRLSDGYVLTDEG 123

Qy 118 LADRATFVWPGQIQAIEVTAEGIGRDAASDLRKIKAQYVASHPGEVCPAKNKEGEAT 177
 | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| |
 Db 124 IAYRGLFLIDGKGVLRQITYVNDLPVGRSVDREALRLVQAFQTDEH-GEVCPAGWKPGSDT 182

Qy 178 LAPSLD 183
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 Db 183 IKPNVD 188

RESULT 6
 US-08-467-265-16
 ; Sequence 16, Application US/08467265
 ; Patent No. 5985612

GENERAL INFORMATION:

APPLICANT: Ni, Jian
 APPLICANT: YU, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey

COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLogy: linear
 MOLECULE TYPE: protein
 STRANDEDNESS: <Unknown>
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 2; Length 257;
 Best Local Similarity 38.5%; Pred. No. 1.8e-32;
 Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Qy 11 FKNQAFKNGERIEITEKDTEGRWSVFFFFPADFTFCVPCTPELGVDADHYELQKGVDY 70
 Db 73 FGKTAGVNGERKELSDDFKGKYLY-LFFPLDFTFVCPCREIVAFSDKANEFHVNCEWV 131

Qy 71 AVSTDTHFTKAWHSSET--IAKIKYAMIGDPGALTNRFDNNRDEGLADRAFVVD 127
 Db 132 AVSVDHFHSLAWINIPRKNGLGHMNITLSDTKOISRDYGVILLESGAGIALRGLFIID 191

Qy 128 POGITOAIEVTAEGIGRDAASDLRKKAQYVASYSPGEVCPAKNGEATLAPS 181
 Db 192 PNGVVKHLSYNDLPVGRSVETRLVKAQFVETH-GEVCPANNTPESPPIKPS 244

RESULT 7
 US-08-467-265-16
 Sequence 16, Application US/08467265
 GENERAL INFORMATION:
 Patent No. 6255079
 APPLICANT: Ni, Jian
 YU, Guo-Liang
 Genitz, Reiner
 Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 4; Length 257;
 Best Local Similarity 38.5%; Pred. No. 1.8e-32;
 Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Qy 11 FKNQAFKNGERIEITEKDTEGRWSVFFFFPADFTFCVPCTPELGVDADHYELQKGVDY 70
 Db 73 FGKTAGVNGERKELSDDFKGKYLY-LFFPLDFTFVCPCREIVAFSDKANEFHVNCEWV 131

Qy 71 AVSTDTHFTKAWHSSET--IAKIKYAMIGDPGALTNRFDNNRDEGLADRAFVVD 127
 Db 132 AVSVDHFHSLAWINIPRKNGLGHMNITLSDTKOISRDYGVILLESGAGIALRGLFIID 191

Qy 128 POGITOAIEVTAEGIGRDAASDLRKKAQYVASYSPGEVCPAKNGEATLAPS 181
 Db 192 PNGVVKHLSYNDLPVGRSVETRLVKAQFVETH-GEVCPANNTPESPPIKPS 244

RESULT 8
 US-09-407-891-16
 Sequence 16, Application US/09407891
 GENERAL INFORMATION:
 PATENT NO. 6254164
 APPLICANT INFORMATION:
 APPLICANT: NI, Jian
 APPLICANT: YU, Guo-Liang
 APPLICANT: Genitz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

STRANDEDNESS:

TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-407-891-16

Query Match

Best Local Similarity 34.2%; Score 337.5; DB 4; Length 257; Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

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Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

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Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

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Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Best Local Similarity 35.6%; Pred. No. 1.3e-31; Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5; Sequence CHARACTERISTICS:

QY 1 MSINTK---KPKNA FKNGERIEITEKDTEGRWSVFFFPADEFFVCPTELGDV 55
Db 1 MSGNAKIGYPAPNEFATAVPDPGQKDPLSPRTIAQDYGVL 59

QY 11 FKNQAFKNGERIEITEKDTEGRWSVFFFPADEFFVCPTELGDVADHYEPLQKGVDVY 70
Db 73 FKGTAVGNGERKEFLSLDDFKGYLV-LFFYPLDFTFVCPCBIVAFSDKANEHFDVNCVV 131

QY 71 AVSTDHFTHKAWHSSET--I AKIYAMIGDPGALTNRNFNMREDEGLADRWFVD 127
Db 132 AVSVPSHFSHLAWNTPRKGNGHNTLISDITRQISROYGVILLESAGIALRGLFIID 191

QY 128 PQGIQKIEVTAEGIGRDAASLLRKIAQVASHRGVEVPAKWBEAATAPS 181
Db 192 PNGVVKILSYNDLPVGRSVEETRLVKAFOFETH-GEVCPANWTPESPIKPS 244

RESULT 9
US-08-467-265-17
; Sequence 17, Application US/08467265

GENERAL INFORMATION:
PATENT NO. 5985612

APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: STUART & OLSSTEIN
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-467-265-17

Query Match 33.3%; Score 329; DB 4; Length 199;
Best Local Similarity 35.6%; Pred. No. 1.3e-31;
Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5;

QY 1 MSLINTK---KPKNA FKNGERIEITEKDTEGRWSVFFFPADEFFVCPTELGDV 55
Db 1 MSGNAKIGYPAPNEFATAVPDPGQKDPLSPRTIAQDYGVL 59

QY 56 ADHYEEQLQKGVVWYAVSTDTHKAWSSET--IAKIYAMIGDPGTGALTNRFDNM 112
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 SDRADFKKLNCQVIGASVDSFCHLAWINTPKQGGLGPMNIPLSDPKRTIQAODGV 119
 QY 113 REDEGLADRATFWVDPQGIQIAEVTAEGIGRDAIDLRLKIKAOVASHPGEVCPAKW 172
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 120 KADEGISFRGLFTIDDKGILROITNDLPVGRSVDEIRLVQAFQFTDKH-GEVCPAGWK 178
 QY 173 EGEATLAPS 183
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 Db 179 PGSDTIKPDV 189

RESULT 11
 US-09-407-891-17
 ; Sequence 17, Application US/09407891
 ; Patent No. 6294164
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE: 06-JUN-1995
 ATTORNEY / AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY / AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 32800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-407-891-17

Query Match 33.3%; Score 329; DB 4; Length 199;
 Best Local Similarity 35.6%; Pred. No. 1.3e-31; Pred. No. 6.7e-31;
 Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5;

QY 1 MSLINKI---KPFKQAA-FKNGEIEETEDTGRMSVFFFVPADEFVCPTELGDV 55
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1 MSGNAKIGHPNPKATAWMPDGQPKDLSIDYKGKY-VVFFYPLDFTFVCPEITAF 59
 QY 56 ADHYEEQLQKGVVWYAVSTDTHKAWSSET--IAKIYAMIGDPGTGALTNRFDNM 112
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 SDRADFKKLNCQVIGASVDSFCHLAWINTPKQGGLGPMNIPLSDPKRTIQAODGV 119
 QY 113 REDEGLADRATFWVDPQGIQIAEVTAEGIGRDAIDLRLKIKAOVASHPGEVCPAKW 172
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 120 KADEGISFRGLFTIDDKGILROITNDLPVGRSVDEIRLVQAFQFTDKH-GEVCPAGWK 178
 QY 173 EGEATLAPS 182
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 Db 179 PGSDTIKPDV 188

RESULT 12
 US-08-299-162A-2
 ; Sequence 2, Application US/08299162A
 ; Patent No. 5610286
 GENERAL INFORMATION:
 APPLICANT: Shau, Hungyi
 ADDRESS: Golub, Sidney H
 STREET: 2029 Century Park East, Suite 3800
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90067
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/299,162A
 FILING DATE: August 31, 1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Oldenkamp, David J
 REFERENCE/DOCKET NUMBER: 104-280
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-277-7800
 TELEFAX: 310-277-1297
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-299-162A-2

Query Match 32.7%; Score 323; DB 1; Length 199;
 Best Local Similarity 36.8%; Pred. No. 6.7e-31;
 Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;

QY 1 MSLINKI---KPFKQAA-FKNGEIEETEDTGRMSVFFFVPADEFVCPTELGDV 55
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1 MSGNAKIGHPNPKATAWMPDGQPKDLSIDYKGKY-VVFFYPLDFTFVCPEITAF 59
 QY 56 ADHYEEQLQKGVVWYAVSTDTHKAWSSET--IAKIYAMIGDPGTGALTNRFDNM 112
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 SDRADFKKLNCQVIGASVDSFCHLAWINTPKQGGLGPMNIPLSDPKRTIQAODGV 119
 QY 113 REDEGLADRATFWVDPQGIQIAEVTAEGIGRDAIDLRLKIKAOVASHPGEVCPAKW 172
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 120 KADEGISFRGLFTIDDKGILROITNDLPVGRSVDEIRLVQAFQFTDKH-GEVCPAGWK 178
 QY 173 EGEATLAPS 182
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 179 PGSDTIKPDV 188

RESULT 13
 US-08-467-265-14

Copyright (c) 1993 - 2000	GenCore version 4.5	Compugen Ltd.
On protein - protein search, using sw model		
Run on:	May 19, 2002, 00:29:30 ; Search time 51.62 Seconds	(without alignments)
Title:	US-09-679-705-24	349.957 Million cell updates/sec
Perfect score:	987	
Sequence:	1 MSLINTRKIKPFPKQAFKNGE..... AKWKEGEATLAPSNDLVGKI 188	
Scoring table:	BLOSUM62	
Gapop 10.0 , Gapext 0.5		
Searched:	283138 seqs, 96089334 residues	
Total number of hits satisfying chosen parameters:	283138	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
	Listing first 45 summaries	
Database :	PIR71: 1: pir1: 2: pir2: 3: pir3: 4: pir4:	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Match Length DB ID
1	970.5	98.3 187 2 JN0289
2	970.5	98.3 187 2 D90709
3	970.5	98.3 187 2 H5559
4	963.5	97.6 187 2 AB0577
5	742.5	75.2 187 2 DB7610
6	677.5	72.3 206 2 GB2668
7	677.5	68.6 187 2 F99583
8	644.5	65.3 189 2 FR9804
9	624.5	63.3 168 2 PS0179
10	622.5	63.1 184 1 A35441
11	612.5	62.1 179 2 S52934
12	605.5	61.3 187 2 C83627
13	603.5	61.1 187 2 A86667
14	488.5	49.5 188 2 D71314
15	455.5	46.1 211 2 G70343
16	365	37.0 242 2 S49173
17	362	36.7 210 2 F06318
18	361	36.6 198 2 A57716
19	354	35.9 265 2 T09211
20	344.5	34.9 198 2 168897
21	338	34.2 219 2 I52425
22	337.5	34.2 257 2 JQ0064
23	334	33.8 199 2 A46711
24	334	33.8 576 2 RT6005
25	330	33.4 203 2 A12385
26	329.5	33.4 200 2 151016
27	329	33.4 199 2 A48513
28	324.5	32.9 195 2 JC2258
29	322.5	32.7 2 G01790
ALIGNMENTS		
RESULT	1	
JN0289		2-cys Peroxiredoxin
N;Alternate names: sulfate starvation-induced protein SSI8		hypothetical prote
C;Species: Escherichia coli		mer5 homolog R07E5
C;Date: 16-Sep-1992 #sequence_revision 30-Sep-1997 #text_change 11-Jun-1999		probable alkyl hyd
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.		hypothetical prote
Science 277, 1453-1462, 1997		2-cys peroxiredoxi
A;Title: The complete genome sequence of Escherichia coli K-12.		thioredoxin peroxi
A;Reference number: A64720; MUID:97426617		probable peroxidas
A;Accession: C64794		antioxidant, Ahpc/
A;Status: nucleic acid sequence not shown; translation not shown		alkyl hydroperoxid
A;Molecule type: DNA		thio-specific anti
A;Residues: 1-187 <BLAT>		thio-specific anti
A;Cross-references: GB:AE000166; GB:U00096; NID:91786819; PID: AAC73706.1; PID:917868		probable alkyl hyd
A;Experimental source: strain K-12, substrain MG1655		alkyl hydroperoxo
R;Ueshima, R.; Fujita, N.; Ishihama, A.		2-cys peroxiredoxi
Biochem. Biophys. Res. Commun. 184, 634-639, 1992		
A;Title: Identification of Escherichia coli proteins cross-reacting with antibodies a		
A;Reference number: JN0286; MUID:92246944		
A;Accession: JN0289		
A;Molecule type: protein		
A;Residues: 2-31 <UES>		
A;Note: this protein fragment has exact coincidence, except 1le-24, with the first 31		
R;Quadroni, M.; Staudenmann, W.; Kertesz, M.; James, P.		
Eur. J. Biochem. 239, 773-781, 1996		
A;Title: Analysis of global responses by protein and peptide fingerprinting of protein		
coll.		
A;Accession number: S78617; MUID:96370830		
A;Accession: S78624		
A;Molecule type: protein		
A;Residues: 2-11 <QUA>		
A;Genetics:		
A;Gene: ahpc		
C;Superfamily: alkyl hydroperoxidase		
C;Keywords: oxidoreductase		
F;2-187/Product: alkyl hydroperoxidase		
F;11-146/Domain: alkyl hydroperoxidase c22 protein homology <C22>		
Query Match 98.3%; Score 970.5; DB 2; Length 187; Best Local Similarity 99.5%; Pred. No. 3e-81; Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1; Qy 1 MSLINTRKIKPFPKQAFKNGEFLIEITEKDTEGRWSVFFYPADEFVCPTELGVDVADHE 60 Db 1 MSLINTRKIKPFPKQAFKNGEFLIEITEKDTEGRWSVFFYPADEFVCPTELGVDVADHE 59		
Qy 61 ELQLGWDWAVSTDTHFTHKAWSSETAKIYKMGDTGALTRNFDNREDEGLAD 120 Db 1 MSLINTRKIKPFPKQAFKNGEFLIEITEKDTEGRWSVFFYPADEFVCPTELGVDVADHE 59		

Db 60 ELQKLGVDVVAVSTDHFTHKAWHSSSETAKIKYAMIGPTGALTNRNFNMREDEGLAD 119
 Qy 121 RATFVVDPOGIIQATEVTAEGIGRASDLRLRKIKAAQYVASHPGEVCPAKWKEGETLAP 180
 Db 120 RATFVVDPOGIIQATEVTAEGIGRASDLRLRKIKAAQYVASHPGEVCPAKWKEGETLAP 179

Qy 181 SLDLVGKI 188
 Db 180 SLDLVGKI 187

RESULT 2
 D97079 alkyl hydroperoxide reductase C22 subunit [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli)

C;Date: 10-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C;Accession: D97079 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gassawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. J.A. Res. 8, 11-22, 2001 Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and geno

A;Reference number: A99629; MUID:2115631; PMID:11258796

A;Accession: D97079 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-187 <HAY>

A;Cross-references: GB:BA000007; PIDN:BAD34067.1; PID:913360102; GSPDB:GN00154

A;Experimental source: strain 0157:H7, substrain RIMD 0509952

C;Genetics:
 A;Gene: Ecs0644

C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
 C;Keywords: oxidoreductase

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
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Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
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Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

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Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
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Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

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Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

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Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

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 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.3%; Score 970.5; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

Matches 187; Conservative 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;

A;Residues: 1-187 <END>
 A;Cross-references: GB:AE005174; NID:912513501; PIDN:AAG54940.1; GSPDB:GN00145; UWGP:Z07
 A;Experimental source: strain 0157:H7, substrain EDI933
 C;Genetics:
 C;Gene: anpC

RESULT 5
 D87610 alkyl hydroperoxide reductase, subunit c [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus
 C;Accession: D87610
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Delsay, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: D87610
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-187 <SLOC>
 A;Cross-references: GB:AE005673; NID:913424540; PIDN:AAK24880.1; GSPDB:GN00148
 C;Genetics:
 A;Gene: C02918
 C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 75.2%; Score 742.5; DB 2; Length 187;
 Best Local Similarity 72.3%; Pred. No. 2e-60; Matches 136; Conservative 27; Mismatches 24; Indels 1; Gaps 1;

QY 1 MSЛИНТКИКРКНQАКНГЕРІТЕІКДТБСРWSVFFFPADFTFVCPTEЛGDYADHYE 60
 Db 1 MSЛINTEIKPKPKNQAKNGERITEIKDTBСRWSVFFFPADFTFVCPTEЛGDYADHYE 59

QY 61 ELQKLGVDWYAVSTDPHFKAWHSSETATIKYAMIGPTGALTRNFDMREBGLAD 120
 Db 61 ELQKLGVDWYAVSTDPHFKAWHSSETATIKYAMIGPTGALTRNFDMREBGLAD 120

QY 121 RATFVUDPOGIIQATEVTAEGTGRDASDLRKKAQYASHPGEVCPAKWEGENTLAP 180
 Db 120 RGTFIILPQGIVLQFMETVAGCIGRNAILLRKKAQYVAHPGEVCPAKWEGENTLAP 179

QY 181 SLDLVGKI 188
 Db 180 SLDLVGKI 187

RESULT 6
 G82668 subunit C of alkyl hydroperoxide reductase XP1530 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
 C;Accession: G82668
 C;Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717
 A;Accession: G82668
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-206 <SIM>
 A;Cross-references: GB:AE003983; GB:AE003849; NID:9106567; PIDN:AAF84339.1; GSPDB:GN001
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aceacio, M.; Alvarenia, R.; A
 Brito, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 ass-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
 J.D.; Jungueira, M.L.; Kemper, E.L.; Kirajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.C.; Miracca, E.C.; Miyaki, C.Y.;
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawsak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 A;Genetics:
 A;Gene: XF1530

C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
 C;Accession: D87610
 R;Best Local Similarity 72.3%; Score 714; DB 2; Length 206;
 R;Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
 R;Best Local Similarity 69.1%; Pred. No. 8.9e-58;
 R;Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
 QY 1 MSЛИНТКИКРКНQАКНГЕРІТЕІКДТБСРWSVFFFPADFTFVCPTEЛGDYADHYE 60
 Db 21 MSVLNTIELSFKATAKNGQFVENSEAVLKSGKWA-FVVFYPADFTFVCPTEЛGDYADHYE 79

QY 61 ELQKLGVDWYAVSTDPHFKAWHSSETATIKYAMIGPTGALTRNFDMREBGLAD 120
 Db 80 ERQKYGVIEYVSVSTDPHFKAWHDISPALGKRYAMIGDPTHEISRNF-NVLRLPSGLAD 138

QY 121 RATFVUDPOGIIQATEVTAEGTGRDASDLRKKAQYASHPGEVCPAKWEGENTLAP 180
 Db 139 RGTFIILPQGIVLQFMETVAGCIGRNAILLRKKAQYVAHPGEVCPAKWEGENTLAP 198

QY 181 SLDLVGKI 188
 Db 199 SLDLVGKI 206

RESULT 7
 F69583 alkyl hydroperoxide reductase (EC 1.6.4.-) small chain - Bacillus subtilis
 N;Alternative names: 5K protein; alkyl hydroperoxide reductase chain C22 homolog; NADH
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C;Accession: F69583, G44519
 R;Kunst, F.; Oasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.;Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.;Erlich, S.D.;Emmerson, P.T.;Entian, K.D.; Errington, J.;Fabret, C.;Ferrari,
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 Y.;M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Satoh, T.; Scanl
 A;Authors: Schlecht, S.; Schroeter, F.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Togoni, A.; Tosato, V.; Uchiya
 T.;Winters, P.;Wipat, A.;Yamamoto, H.;Yamane, K.;Yasumoto, K.;Yata, K.;Yoshida
 A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.;Danchin, A.;
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
 A;Reference number: A69580; MUID:98044033
 A;Accession: F69583
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-187 <KUN>
 A;Cross-references: GB:Z99124; GB:AL009126; NID:92636442; PID: CAB16046.1; PID:926365
 A;Experimental source: strain 168
 R;Dowds, B.C.A.
 submitted to the Protein Sequence Database, February 1993
 A;Reference number: A44519
 A;Accession: G44519
 A;Molecule type: Protein
 A;Residues: 2-36, XX, 39-41 <DOW>
 C;Genetics:
 A;Gene: ahpc
 C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
 C;Keywords: NAD; oxidoreductase
 F;2-187/Product: alkyl hydroperoxide reductase small chain #status predicted <MAT>
 F;11-144/Domain: alkyl hydroperoxidase c22 protein homology <C22>
 Query Match 68.6%; Score 677.5; DB 2; Length 187;
 Best Local Similarity 64.9%; Pred. No. 1.7e-54;
 Matches 122; Conservative 32; Mismatches 33; Indels 1; Gaps 1;
 C;Genetics:
 QY 1 MSЛИНТКИКРКНQАКНГЕРІТЕІКДТБСРWSVFFFPADFTFVCPTEЛGDYADHYE 60
 |||| :: ||: :|||||:|||: :||:||| :|||:|||: :|||:|||: :|||:|||: :|||:|||: :|||:|||: :|||:

Db 1 MSLIGKEVLPPFREAKKNGERIDVNTNEDLKQWWSV-FCFWYPADFSVCPTLELDIQLQYQA 59
 C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
 F;1-130/Domain: alkyl hydroperoxidase c22 protein homology (fragment) <C22>
 Qy 61 ELOKIGKVGVYAVSTDHFTHKAWHSSETAKIKYAMIGPTGALTRNFNDNMREDEGLAD 120
 C;Species: Bacillus sp.
 Db 60 ALKELGVEVYVSSTDHFVHKGWHDSSSEKISKITVAMGDPSPOTISRNFDVLDIETGLAD 119
 C;Accession: PS0179 1 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
 Qy 121 RATFVVDPOGIIQAIETAEGIGRASDLIRKIKAAQYVASHRHPGEVCPAKWKEGEATLAP 180
 Db 120 RGFTTIDPGVYIOTVEINAGGGRDASLNVKVKAQYVQRNPGEVCPAKWEEGETLIP 179
 Qy 181 SLDLVGKI 188
 Db 180 SLDLVGKI 187

RESULT 8
 F89804 alkyl hydroperoxide reductase subunit C [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus*
 C;Description: Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: F89804
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID: 21311952; PMID: 11418146
 A;Accession: F89804
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-189 <KUR>
 A;Cross-references: GB:BA000018; PID:gi13700295; PIDN:BAB41593.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: ahpc
 C;Superfamily: alkyl hydroperoxide reductase subunit C [imported] - *Staphylococcus aureus* (strain N315)

Query Match 65.3%; Score 644.5.; DB 2; Length 189;
 Best Local Similarity 64.2%; Pred. No. 1.8e-51;
 Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

Qy 1 MSLINRKPKRNQAF--KNGEPIETTEKDEPGRNSVFFFYPADEFVCPTELDVADH 58
 Db 1 MSLINKEILPPTAQARDPKKQDFKEVQEDLKGWSV-VCFYPADESFVCPTELEDLQNO 59

Qy 59 YEELOKLGVYVAASDTHFTHKAWHSSETAKIKYAMIGPTGALTRNFNDNMREDEGL 118
 Db 60 YEELOKLGVYVFSVSTDHFVHKAWHDHSDAISKITYTMIGDPSPOTIRNFNDVLDIETGL 119

Qy 119 ADRTFVVDPOGIIQAIETAEGIGRASDLIRKIKAAQYVASHRHPGEVCPAKWKEGEATL 178
 Db 120 AQRGFIIDPGVYQASEINADGIGRDASTLAHKIKAAQYVQRNPGEVCPAKWEECAKTL 179

Qy 179 APSLDLVGKI 188
 Db 180 QPGLDLVGKI 189

RESULT 9
 PS0179 hypothetical protein (ndh 5' region) - *Bacillus* sp. (fragment)
 C;Species: *Bacillus* sp.
 Db 1 MSLINRKPKRNQAF--KNGEPIETTEKDEPGRNSVFFFYPADEFVCPTELDVADH 60

Qy 1 MSLINRKPKRNQAF--KNGEPIETTEKDEPGRNSVFFFYPADEFVCPTELDVADH 59
 Db 1 MSLINRKPKRNQAF--KNGEPIETTEKDEPGRNSVFFFYPADEFVCPTELDVADH 60

Qy 61 ELOKIGKVGVYAVSTDHFTHKAWHSSETAKIKYAMIGPTGALTRNFNDNMREDEGLAD 120
 Db 60 ELOKIGKVGVYAVSTDHFTHKAWHSSETAKIKYAMIGPTGALTRNFNDNMREDEGLAD 119

A;Title: Nucleotide sequence of the gene encoding NADH dehydrogenase from an alkalophile
 A;Reference number: JX0166; MUID: 92011449
 A;Accession: PS0179
 A;Molecule type: DNA
 A;Residues: 1-168 <KUR>
 A;Experimental source: strain YN-1

RESULT 11
 S52934 alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - *Staphylococcus aureus* (fragm
 C;Species: *Staphylococcus aureus*
 C;Date: 06-Jun-1995 #sequence_revision 22-May-1998 #text_change 17-Jul-1998

C;Accession: S52934
R;Through, J.P.; Armstrong-Buisseret, L.; Cole, M.B.; Stewart, G.S.A.B.
Submitted to the EMBL Data Library, February 1995
A;Description: A homologue of the Escherichia coli hydroperoxide reductase Ahpc is induced by Accession: S52934
A;Molecule type: DNA
A;Residues: 1-179 <THR>
A;Cross-references: EMBL:X85029
A;Experimental source: strain RNA4220
C;Genetics:
A;Gene: ahpc
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot
F;1-138/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 62.1%; Score 612.5; DB 2; Length 179;
Best Local Similarity 63.9%; Pred. No. 1.4e-48; Mismatches 38; Indels 3; Gaps 2;
Matches 115; Conservative 24; Db 180 SLDLVSKI 187

RESULT 13
Qy 11 FKNQAF--KNGEFEITTEKDGEGRMSVFFFYPADETFVCPTELGVDVADYELQKLGVD 68
Db 1 FTAQAFDPKKDQPKVQDPLGKGSV-VCFYPADFSVCPTELQDQYELQKLGVN 59

Qy 69 VVAVSTIDTHFKAWHSSETAKIKYAMIGDPTGALTRNFNDNMREDEGLADARATFVDP 128
Db 60 VFSVSDTHTHVKAWHDSDALKSITVMTGDPSPOTIRBDVLDATGLAQRGFIIDP 119

Qy 129 QGIIQIAAEVTAEGIGRDAASDLRKTKAAQYVASHPGEVCAKWKGEATLAPSIDLVGI 188
Db 120 DGVVVAOSEINADGIGRDASTLAHKKAQYVVRKNPGEVCPAKWEGAKTLQPGDLVGI 179

RESULT 12
C83627 alkyl hydroperoxide reductase subunit C PA0139 [Imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa
C;Date: 12-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83627
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 405, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:2043737
A;Accession: C83627
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <STO>
A;Cross-references: GB:AE004452; GB:AE004091; NID:9945968; PIDN:AAG03529.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: ahpc; PA0139
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 61.1%; Score 603.5; DB 2; Length 187;
Best Local Similarity 58.5%; Pred. No. 9.6e-48; Mismatches 44; Indels 1; Gaps 1;
Matches 110; Conservative 33; Db 181 SLDLVSKI 188

RESULT 14
D71314 probable alkyl hydroperoxide reductase (ahpc) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 11-Jun-1999
C;Accession: D71314
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Pearson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Gill, S.; Weiland, J.; Smith, H.O.; Ventier, J.C.
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Accession: D71314
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-188 <COL>
A;Cross-references: GB:AE001227; GB:AE000520; NID:9332279; PIDN: AAC65497.1; PID:9332
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0509
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 49.5%; Score 488.5; DB 2; Length 188;
Best Local Similarity 49.7%; Pred. No. 3e-37; Mismatches 61; Indels 1; Gaps 1;
Matches 93; Conservative 32; Mismatches 61; Db 180 SLDLVSKI 187

Query Match 49.5%; Score 488.5; DB 2; Length 188;
Best Local Similarity 49.7%; Pred. No. 3e-37; Mismatches 61; Indels 1; Gaps 1;
Matches 93; Conservative 32; Mismatches 61; Db 180 SLDLVSKI 187

Qy 61 BLQKLGVDVAVSTIDTHFKAWHSSETAKIKYAMIGDPTGALTRNFNDNMREDEGLAD 120
Db 60 EFOKAGAAEVYTIVTDFHESKWHPSVPAVGKAQPLIGDPTQHDTNAFVHPEGLAL 119

Qy 121 RATVVDPQGTIAQATEVARGIGRDAASDLRKTKAAQYVASHPGEVCPAKWKEGETLAP 180
Db 120 RGFVINPEGVKTBHNSNEARDQGETVRLKKAQYTAHHPGEVCPAKWKEGETLAP 179

QY 2 SLINTRIKPKFKNQAFRNGEFTETEKDEGKWSVFFFPADFTFVCPTELGVDADHYEE 61
 ||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 3 SLIGRKVIDFKLPATVGGKTFEVNASIKGSWAN-FMFYPADEFIVCPTELADLARVPS 61
 QY 62 LQKLGDVWAVSTDFHFTHAWHSSETIHKIKYAMIGDDTGALTRNFEDNREDEGLADR 121
 ||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 62 FVEIGCKVSVSTDSKVHKAADATDTIKNLPYEMISDKAGKLAGFFGVILPDAWHALR 121
 QY 122 ATFWVDPQGIQAIETAEIGGRASDLRLRKIAQYASHPGEVCPAKWKEGEATLAPS 181
 ||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 122 GTFWVDPPEGLVKAFEVHDMGIGRADELLRKVSQFVAKRGDQCPARURPKAKTLKG 181
 QY 182 LDLVGKI 188
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 Db 182 IDLGKI 188

RESULT 15

70343 alkyl hydroperoxide reductase - Aquifex aeolicus

C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
 C;Accession: G70343
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
 V;Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:9819666
 A;Accession: G70343
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-211 <AOF>
 A;Cross-references: GB:AE000692; NID:g2983130; PID:AC06735.1; PID:g2983132; GB:AE00065
 A;Experimental source: strain VF5
 C;Genetics:
 A;Gene: ahpc1
 C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 prot

Query Match 46.1%; Score 455.5; DB 2; Length 211;
 Best Local Similarity 45.0%; pred. No. 3.6e-34;
 Matches 85; Conservative 41; Mismatches 58; Indels 5; Gaps 3;

QY 4 INTKIKPFKNQAF- KNGEFIEITEKD- -TEGRWSVFFFPADFTFVCPTELGVDADHY 59
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 18 VGQKVNPNEMETYDPSTGKGKVYLDLKKRW-VILEFPADFTFVCPTELGADAEKY 76
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 QY 60 EBLQKLGDVWAVSTDFHFTHAWHSSETIHKIKYAMIGDDTGALTRNFEDNREDEGLA 119
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 77 DELKEMCEVIVSSTDFKVLHLWRDEPLKVNYPGMADPTGQVSLFLFGVYDENTGLA 136
 QY 120 DRATFWVDPQGIQAIETAEIGGRASDLRLRKIAQYASHPGEVCPAKWKEGEATL 179
 ;| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 137 LRGTFLINPSEGVLVGSEVNFYINVGRNADELVRMKANVYLMSPHEECPAKWEPGKRLK 196
 QY 180 PSLDLVGKI 188
 ;|| :|||:
 Db 197 PSEELVGRV 205

Copyright (c) 1993 - 2000	GenCore version 4.5	Compugen Ltd.
OM protein - protein search, using sw model		
Run on:	May 19, 2002, 00:31:21 ;	Search time 40.11 Seconds
		(without alignments)
		181.483 Million cell updates/sec
Title:	US-09-679-705-24	
Perfect score:	987	
Sequence:	1 MSLINTRKPKFKNQAFKNGE AKWKKGAEATLAPSILDVGKI 188	
Scoring table:	BLOSUM62	
	Gapop 10.0 , Gapext 0.5	
Database :	SwissProt_40:*	
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
		SUMMARIES
Result No.	Score	Query Match Length DB ID
1	965.5	97.8 186 1 AHPC_ECOLI
2	958.5	97.1 186 1 AHPC_SALTY
3	677.5	68.6 187 1 AHPC_BACSU
4	624.5	63.3 168 1 YNDH_BACSP
5	366.5	37.1 266 1 BASI_ARATH
6	362	36.7 210 1 BASI_WHEAT
7	361	36.6 198 1 PDX2_RAT
8	361	36.6 210 1 BASI_HORVU
9	358.5	36.3 198 1 PDX2_MOUSE
10	354	35.9 265 1 BASI_SP10L
11	346.5	35.1 256 1 PDX3_HUMAN
12	343.5	34.8 198 1 PDX2_HUMAN
13	338	34.2 199 1 PDX1_RAT
14	337.5	34.2 257 1 PDX3_MOUSE
15	335.5	34.0 257 1 PDX3_BOVIN
16	334	33.8 199 1 PDX1_HUMAN
17	330.5	33.5 199 1 TDX2_BRUMA
18	329.5	33.4 200 1 TDX1_CPNPY
19	329	33.3 199 1 PDX1_MOUSE
20	322.5	32.7 271 1 PDX4_HUMAN
21	322	32.6 229 1 TDX1_BRUMA
22	321.5	32.6 274 1 PDX4_MOUSE
23	312	31.6 199 1 YC42 PORPU
24	312	31.6 226 1 TDX1_GAEL
25	307	31.1 200 1 Y755_SYN3
26	305.5	31.0 199 1 TDX1_TRIBR
27	291.5	29.5 194 1 TDX_FASHE
28	29.5	200 1 TDX_ONCNY
29	285.5	28.9 196 1 TSAL_CANAL
30	266	27.0 233 1 CR29_ENTHI
31	265.5	26.9 178 1 R20K_CLOPA
32	26.5	204 1 YC42_OPSSI
33	258.5	195 1 TSA2_YEAST

RESULT	1	ALIGNMENTS
AHPC_ECOLI		
ID AHPC_ECOLI	STANDARD;	PRT; 186 AA.
AC P26427;		
DT 01-AUG-1992 (Rel. 23, Created)		
DT 01-JUN-1994 (Rel. 29, Last sequence update)		
DT 01-MAR-2002 (Rel. 41, Last annotation update)		
DE Alkyl hydroperoxide reductase C22 Protein (EC 1.6.4.-) (SCRB-23)		
DE (Sulfate starvation-induced protein 8) (SSIB).		
DE AHPC OR B0605 OR Z0749 OR ECS0644.		
OS Escherichia coli, and		
OS Escherichia coli O157:H7.		
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
OC Escherichia.		
OX NCBI_TaxID=562, 83334;		
RP [1]		
SEQUENCE FROM N.A.		
RN		
RC STRAIN=K12;		
RX MEDLINE=92276370; PubMed=1592833;		
RA Smillie D.A., Hayward R.S., Suzuki T., Fujita N., Ishihama A.; "Locations of genes encoding alkyl hydroperoxide reductase on the physical map of the Escherichia coli K-12 genome.";		
RT J.Bacteriol. 174:3826-3827(1992).		
RL		
RC		
SEQUENCE FROM N.A.		
[2]		
STRAIN=K12 / MG1655;		
RX MEDLINE=97426617; PubMed=9278503;		
RX Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J.J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Maurer B., Shao Y.; "The complete genome sequence of Escherichia coli K-12.";		
RT Science 277:1453-1474(1997).		
RL [3]		
SEQUENCE FROM N.A.		
RX Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Lin D., Feddersen N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R. W.; Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.		
RN [4]		
SEQUENCE FROM N.A.		
RX STRAIN=K12;		
RC STRAIN=97061202; PubMed=8905232;		
RX Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Kishimoto K., Inada T., Itch T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horikuchi T.; "A 77-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";		
RT DNA Res. 3:137-155(1996).		
RN [5]		
SEQUENCE FROM N.A.		
RX R20K_CLOPA		
RX P23161 clostidium		
RX P49537 odontella s		
RX Q04120 saccharomyces		
RX MEDLINE=21074935; PubMed=11206551;		

RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotnick E.J., Davis N.W., Lim A., Dimaranta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL *Nature* 409:529-533 (2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 059952;
 RX MEDLINE=21156231; PubMed=11258796;
 DR EMBL; AE000166; AAC7706.1; -.
 DR EMBL; U82538; AAB4806.1; -.
 DR EMBL; D90702; BAA3244.1; -.
 DR EMBL; D90701; BAA35235.1; -.
 DR EMBL; AE005240; AAG54940.1; -.
 DR EMBL; AP002552; BAB34067.1; -.
 DR PIR; JN0289; JN0289.
 DR HSSP; P30041; IPRX.
 DR SWISS-2DPAGE; P26427; COLI.
 DR ECO2DBASE; B020_9; 6TH EDITION.
 DR Ecogene; EG11384; ahpc.
 DR InterPro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW oxidoreductase; Complete proteome.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 46 46 BY SIMILARITY.
 FT ACT_SITE 165 165 BY SIMILARITY.
 SQ SEQUENCE 186 AA; 20630 MW; 40CDR2D344CA196B CRC64;

RT antibodies against region 2.2 peptide of RNA polymerase sigma
 RT subunit;";
 RL Biochem. Biophys. Res. Commun. 184:634-639(1992).
 RN [8]
 RP SEQUENCE OF 1-13.

RC STRAIN=K12 / W3110;
 RA Pasquali C., Sanchez J.-C., Ravinder F., Golaz O., Hughes G.J.,
 RA Frutiger S., Pequette N., Wilkins M., Apel R.D., Bairoch A.,
 RA Hochstrasser D.F.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 RN [9]
 SEQUENCE OF 1-27 AND 69-80.

RC STRAIN=K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of *Escherichia coli* K-12.;"
 RL Electrophoresis 18:1259-1313(1997).
 RN [10]
 RP SEQUENCE OF 1-20.
 RC STRAIN=K12;
 RX MEDLINE=95081923; PubMed=7499381;
 RA Cha M.-K., Kim H.-K., Kim I.-H.,
 RT "Thioredoxin-linked 'thiol peroxidase' from periplasmic space of
 Escherichia coli.;"
 J. Biol. Chem. 270:28635-28641(1995).
 RN [11]
 RP SEQUENCE OF 1-10.

RC STRAIN=K12 / MC4100;
 RX MEDLINE=96370830; PubMed=8774726;
 RA Quadroni M., Staudermann W., Kertesz M., James P.;
 RT "Analysis of global responses by protein and peptide fingerprinting
 of proteins isolated by two-dimensional gel electrophoresis. Application to the sulfate-starvation response of *Escherichia coli*.";
 RL Eur. J. Biochem. 238:773-781(1996).
 CC -1- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
 CC DITHIOL FORM.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- PTM: THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 H(2)O(2), AND THE OXIDIZED CYS-46 (PROBABLY CYS-S-OH) RAPIDLY
 REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
 INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 BY THIOREDOXIN.
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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 DR D13187; BAA02485.1; -.
 DR EMBL; DR02538; AAB4806.1; -.
 DR EMBL; D90702; BAA3244.1; -.
 DR EMBL; D90701; BAA35235.1; -.
 DR EMBL; AE005240; AAG54940.1; -.
 DR EMBL; AP002552; BAB34067.1; -.
 DR PIR; JN0289; JN0289.
 DR HSSP; P30041; IPRX.
 DR SWISS-2DPAGE; P26427; COLI.
 DR ECO2DBASE; B020_9; 6TH EDITION.
 DR Ecogene; EG11384; ahpc.
 DR InterPro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW oxidoreductase; Complete proteome.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 46 46 BY SIMILARITY.
 FT ACT_SITE 165 165 BY SIMILARITY.
 SQ SEQUENCE 186 AA; 20630 MW; 40CDR2D344CA196B CRC64;

Query Match 97.8%; Score 965.5; DB 1; Length 186;
 Best Local Similarity 99.5%; Pred. No. 7. 9e-80; 0; Mismatches 0; Indels 1; Gaps 1;
 Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 SLINTKIKPPKKQQAKFRNKGFEIITEKOTEGRWSVVFYIADFTFVCPTEGLGDVADHYEE 61
 Db 1 SLINTKIKPKRNQAKFRNKGFEIITEKOTEGRWSVVFYIADFTFVCPTEGLGDVADHYEE 59
 Qy 62 LQKLGYDVAYSTDHTHKAWSSETAKIYAMIGDPGALTRNFNDNREDEGLADR 121
 Db 60 LQKLGYDVAYSTDHTHKAWSSETAKIYAMIGDPGALTRNFNDNREDEGLADR 119
 Qy 122 ATFWVDPQGIIQIAEVTAEGIGRDASSLRKIAQYVASHPGEVCPAKNKEGEATLAPS 181
 Db 120 ATFWVDPQGIIQIAEVTAEGIGRDASSLRKIAQYVASHPGEVCPAKNKEGEATLAPS 179
 Qy 182 LDLVGKI 188
 Db 180 LDLVGKI 186

RESULT 2
 AHPC-SALTY
 ID AHPC-SALTY STANDARD; PRT; 186 AA.
 AC P19479;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alkyl hydroperoxide reductase C22 Protein (EC 1.6.4.-).
 GN AHPC OR STM0608 OR Smy0633;
 OS *Salmonella typhimurium*, and
 OC *Salmonella typhi*.
 OC *Bacteriia*; *Proteobacteria*; *gamma subdivision*; *Enterobacteriaceae*;
 OC *Salmonella*.
 OX NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=tymphimurium; STRAIN=TN1379;
 RX MEDLINE=9028183; PubMed=2191951;
 RA Tartaglia L.A., Storz G., Brodsky M.H., Lai A., Ames B.N.;
 RT "Alkyl hydroperoxide reductase from *Salmonella typhimurium*. Sequence
 and homology to thioredoxin reductase and other flavoprotein
 disulfide oxidoreductases";
 RL J. Biol. Chem. 265:10535-10540(1990).
 RN [2]
 RP REVISTONS TO C-TERMINUS.
 RC SPECIES=S.typhimurium;
 RX MEDLINE=94316629; PubMed=8041738;

RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;
 RT "Cloning and sequencing of thiol-specific antioxidant from mammalian
 brain: alkyl hydroperoxide reductase and thiol-specific antioxidant
 define a large family of antioxidant enzymes";
 RT proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).
 [3]
 RN SEQUENCE FROM N.A.
 RP SPECIES=S typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RC MEDLINE=21534948; PubMed=2116609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrelle P.,
 Courtney L., Porwollik S., Ali J.J., Dante M., Du F., Hou S., Layman D.,
 Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.;"
 RL Nature 413:852-856(2001).
 RN [4]
 RP SEQUENCE OF 1-20 FROM N.A.
 RC SPECIES=S typhimurium;
 MEDLINE=90133925; PubMed=2693740;
 RA Tartaglia L.A., Storz G., Ames B.N.;
 RT "Identification and molecular analysis of oxyR-regulated promoters
 involved for the bacterial adaptation to oxidative stress.,"
 RL J. Mol. Biol. 210:709-719(1989).
 RN [5]
 RP SEQUENCE OF 1-24.
 RC SPECIES=S typhimurium; STRAIN=OXYR1;
 MEDLINE=89109157; PubMed=2643600;
 RA Jacobson P.S., Morgan R.W., Christian M.F., Ames B.N.;
 RT "An alkyl hydroperoxide reductase from *Salmonella typhimurium*
 involved in the defense of DNA against oxidative damage. Purification
 and properties";
 RT J. Biol. Chem. 264:1488-1496(1989).
 RL [6]
 RN SEQUENCE FROM N.A.
 RP SPECIES=S typhi; STRAIN=CPI8;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks D., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jaelens K.,
 RA Krogh A., Larsen T.S., Leather S., Moulé S., O Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 enterica serovar Typhi CPI8.,"
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: DIRECTLY REDUCES ALKYL HYDROPEROXIDES WITH THE USE OF
 ELECTRONS DONATED BY THE 57 KDA FLAVOPROTEIN ALKYL HYDROPEROXIDE
 CC REDUCTASE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- PIM: THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 H(2)O(2), AND THE OXIDIZED CYS-46 (PROBABLY CYS-SOH) RAPIDLY
 REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
 INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDOXIN.
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC
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 CC
 DR HSSP; P30041; IPRX.
 DR StyGene; SG10004; apcC.
 DR Interpro; IPR00865; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Oxidoreductase; Complete proteome.
 RN INIT_MET 0
 FT ACT_SITE 0
 FT ACT_SITE 46 46 BY SIMILARITY.
 FT ACT_SITE 165 165 BY SIMILARITY.
 FT CONFLICT 1 1 S -> G (IN REF. 5).
 FT CONFLICT 4 4 N -> D (IN REF. 5).
 FT CONFLICT 13 13 O -> N (IN REF. 5).
 FT CONFLICT 16 16 K -> H (IN REF. 5).
 FT CONFLICT 19 19 E -> H (IN REF. 5).
 FT CONFLICT 22 22 E -> S (IN REF. 5).
 SQ SEQUENCE 186 AA; 20616 MW; 83D48A7A667FF5DB0 CRC64;

Query	Match	Score	DB	Length
Best Local Matches	Similarity	97.1%	DB 1;	186;
183;	Conservative	97.9%	Pred. No. 3.4e-79;	0;
	Mismatches	3;	Indels	1;
	Gaps	1;		
OY	2 SLINKIKPFKNQAFKNGEFEITEKDTGEGRMSVFFPPADFTFCPTELGDVADHEE	61	Db	1 SLINKIKPFKNQAFKNGEFEITEKDTGEGRMSVFFPPADFTFCPTELGDVADHEE 59
OY	62 LQKLGVDVYAVSTDTHTPKWAHSSSETITAKIYAMIGDPGALTNRNFNREDEGLADR	121	Db	60 LQKLGVDVYAVSTDTHTPKWAHSSSETITAKIYAMIGDPGALTNRNFNREDEGLADR 119
OY	122 ATFVVVPQGIIQIAETTAEGGRDASDLRLTIKAQAOYVASHPGEVCPAKRKEGEATLAPS	181	Db	120 ATFVVVPQGIIQIAETTAEGGRDASDLRLTIKAQAOYVASHPGEVCPAKRKEGEATLAPS 179
OY	182 LDIVGKI 188	182	Db	180 LDIVGKI 186
Db	180 LDIVGKI 186			
RESULT 3				
AHPC_BACSU				
ID AHPC_BACSU				
STANDARD; PRT; 187 AA.				
AC P80239; P53562;				
DT 01-FEB-1995 (Rel. 31. Created)				
DT 01-OCT-1996 (Rel. 34. Last sequence update)				
DT 16-OCT-2001 (Rel. 40. Last annotation update)				
DE Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-) (General stress protein 22).				
GN AHPC.				
OS <i>Bacillus subtilis</i> .				
OC Bacteria; Firmicutes; <i>Bacillus</i> / <i>Clostridium</i> group;				
OC <i>Bacillus</i> / <i>Staphylococcus</i> group; <i>Bacillus</i> .				
OX NCBI_TaxID=1423;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=168;				
RA Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;				
RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.				
RN [2]				
RP SEQUENCE OF 1-41.				
RC STRAIN=168 / YB86;				
RX MEDLINE=94236234; PubMed=3180695;				
RA Hartford O.M., Dowd B.C.A.;				
RT "Isolation and characterization of a hydrogen peroxide resistant mutant of <i>Bacillus subtilis</i> ."				
RL Microbiology 140:297-304(1994).				
RN [3]				
RP SEQUENCE OF 1-14.				
RC STRAIN=ISB.				
CC MEDLINE=94282319; PubMed=8012595;				
DR Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,				
DR Schmid R., Mach H., Hecker M.,				
DR "Analysis of the induction of general stress proteins of <i>Bacillus subtilis</i> ."				
DR subtilis.;"				
DR PIR; S07525; S07525.				

CC J. Biochem. 109-678-683 (1991).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC PTM: THE CYS-28-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O2, AND THE OXIDIZED CYS-28 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-147-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDOXIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC
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 CC
 CC EMBL: D10701; BRA01544.1;
 DR PIR: PS0179; PS0179.
 DR InterPro: IPR000866; AHPC-TSA.
 DR Pfam: PF00578; AhpC-TSA. 1.
 KW Hypothetical protein; Antioxidant.
 FT ACT_SITE 1 BY SIMILARITY.
 FT ACT_SITE 28 BY SIMILARITY.
 FT NON_TER 1 BY SIMILARITY.
 SEQUENCE 168 AA; 18479 MW; 2D5BC57BB7726CDE CRC64;
 Query Match 63.3%; Score 624.5; DB 1; Length 168;
 Best Local Similarity 67.5%; Pred. No. 3e-49; DB 1;
 Matches 114; Conservative 25; Mismatches 29; Indels 1; Gaps 1;
 QY 20 EFEITEKEDEGRMSVFFPFYPADEFPCPTELGQVADHFEELQKLGDVVAVSTDPTHT 79
 Db 1 EFEIEVEESFRKGQWNS-LCFYPADFTFCVCPTELEDQNVEALKELGVEVASFADSTDPHT 59
 QY 80 HKAWHSSESETIAKIKYAMIGDPGPTGALTRNFDNMREDEGLADRATFWVDPGIQATEVTA 139
 Db 60 HKGNHDSSESPIGKITYAMIGDPGQTSRNFVNLNEVSGLADRGTIFDPDSVWQAELINA 119
 QY 140 EGIGRDASDLRKTAQQYVASHPSQEVCAKWKGEBATLAPSLDLVGKI 188
 Db 120 EGIGRDASDLVKINKAKAQYVNRNPGEVCVCPAKWQEGDETLPASLDLVGKI 168

RESULT	5
BASLARATH	
ID	BASLARATH
AC	Q9291; P92938; Q9570;
DT	01-NOV-1997 (Rel. 35, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	2-cys peroxiredoxin BASL, chloroplast precursor.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis; OX NCBL-TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV_COLUMBIA;
RA	MEDLINE:97408940; PubMed=9263459;
RA	Baier M., Diez K.-J.;
RT	"2-Cys peroxiredoxin basl from <i>Arabidopsis thaliana</i> .";
RL	(In) Plant Gene Register PGR96-031.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV_COLUMBIA;
RA	Baier M., Diez K.-J.;
RT	"The plant 2-cys peroxiredoxin basl is a nuclear-encoded chloroplast protein: its expressionional regulation, phylogenetic origin, and implications for its specific physiological function in plants.;"
RL	(In) Plant Gene Register PGR96-031.

Plant J. 12:179-190(1997).
 [3] DR InterPro; IPR000866; AhPC-TSA.
 RN Pfam; PR00578; AhPC-TSA; 1.
 RP Antioxidant; Chloroplast; Transit peptide.
 RA KW CHIROPPLAST (BY SIMILARITY).
 RL TRANSIT 1
 FT 65
 CHAIN 66 266
 ACT_SITE 119 2-CYS PEROXIREDOXIN BASI.
 FT 119 BY SIMILARITY.
 FT 241 BY SIMILARITY.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salancikat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Perez-Alonso M., Obermaier B.,
 RA Fartmann B., Valie G., Grivelle L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Delseny M., Boutry M., Grivelle L.A., Mache R., Puigdomenech P.,
 RA Wurmbach E., Draneck H., Erffle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Palavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsieck G.,
 RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottewaelde B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Goret P., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.-X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shear T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S.,
 RA Pai G., Millscheer J., Seilers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Saizberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanebe A., Yamada M., Yasuda M., Tabata S.,
 RA RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:820-822(2000).
 RN [5]
 RP SEQUENCE FROM N_A.
 RA Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,
 RA Becker J.;
 RT "Full length cDNA sequence of Arabidopsis thaliana.";
 RL SUBMITTED (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE
 DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF. INVOLVED IN THE
 DETOXIFICATION OF ALKYL HYDROPEROXIDES. EXPRESSION IS RERESSED IN
 RESPONSE TO A HIGHLY REDUCED CELLULAR THIOL POOL, AND SLIGHTLY
 INDUCED BY OXIDATIVE STRESS.
 CC -I- SUBUNITS: HOMODIMER (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -I- PTM: THE CYS-119-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 H2O2(O2), AND THE OXIDIZED CYS-119 (PROBABLY CYS-SOH) RAPIDLY
 REACTS WITH CYS-241-SH OF THE OTHER SUBUNIT TO FORM AN
 INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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DR InterPro; IPR000866; AhPC-TSA.
 DR Pfam; PR00578; AhPC-TSA; 1.
 RP Antioxidant; Chloroplast; Transit peptide.
 RA KW CHIROPPLAST (BY SIMILARITY).
 RL TRANSIT 1
 FT 65
 CHAIN 66 266
 ACT_SITE 119 2-CYS PEROXIREDOXIN BASI.
 FT 119 BY SIMILARITY.
 FT 241 BY SIMILARITY.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salancikat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Perez-Alonso M., Obermaier B.,
 RA Fartmann B., Valie G., Grivelle L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Delseny M., Boutry M., Grivelle L.A., Mache R., Puigdomenech P.,
 RA Wurmbach E., Draneck H., Erffle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Palavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsieck G.,
 RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottewaelde B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Goret P., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.-X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shear T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S.,
 RA Pai G., Millscheer J., Seilers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Saizberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanebe A., Yamada M., Yasuda M., Tabata S.,
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 RT "Full length cDNA sequence of Arabidopsis thaliana.";
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 DETOXIFICATION OF ALKYL HYDROPEROXIDES. EXPRESSION IS RERESSED IN
 RESPONSE TO A HIGHLY REDUCED CELLULAR THIOL POOL, AND SLIGHTLY
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 CC -I- SUBCELLULAR LOCATION: CHLOROPLAST.
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 CC -I- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

DR InterPro; IPR000866; AhPC-TSA.
 DR Pfam; PR00578; AhPC-TSA; 1.
 RP Antioxidant; Chloroplast; Transit peptide.
 RA KW CHIROPPLAST (BY SIMILARITY).
 RL TRANSIT 1
 FT 65
 CHAIN 66 266
 ACT_SITE 119 2-CYS PEROXIREDOXIN BASI.
 FT 119 BY SIMILARITY.
 FT 241 BY SIMILARITY.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salancikat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Perez-Alonso M., Obermaier B.,
 RA Fartmann B., Valie G., Grivelle L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Delseny M., Boutry M., Grivelle L.A., Mache R., Puigdomenech P.,
 RA Wurmbach E., Draneck H., Erffle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Palavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsieck G.,
 RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottewaelde B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Goret P., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.-X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shear T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S.,
 RA Pai G., Millscheer J., Seilers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Saizberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanebe A., Yamada M., Yasuda M., Tabata S.,
 RA RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:820-822(2000).
 RN [5]
 RP SEQUENCE FROM N_A.
 RA Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,
 RA Becker J.;
 RT "Full length cDNA sequence of Arabidopsis thaliana.";
 RL SUBMITTED (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE
 DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF. INVOLVED IN THE
 DETOXIFICATION OF ALKYL HYDROPEROXIDES. EXPRESSION IS RERESSED IN
 RESPONSE TO A HIGHLY REDUCED CELLULAR THIOL POOL, AND SLIGHTLY
 INDUCED BY OXIDATIVE STRESS.
 CC -I- SUBUNITS: HOMODIMER (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -I- PTM: THE CYS-119-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 H2O2(O2), AND THE OXIDIZED CYS-119 (PROBABLY CYS-SOH) RAPIDLY
 REACTS WITH CYS-241-SH OF THE OTHER SUBUNIT TO FORM AN
 INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

DR InterPro; IPR000866; AhPC-TSA.
 DR Pfam; PR00578; AhPC-TSA; 1.
 RP Antioxidant; Chloroplast; Transit peptide.
 RA KW CHIROPPLAST (BY SIMILARITY).
 RL TRANSIT 1
 FT 65
 CHAIN 66 266
 ACT_SITE 119 2-CYS PEROXIREDOXIN BASI.
 FT 119 BY SIMILARITY.
 FT 241 BY SIMILARITY.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salancikat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Perez-Alonso M., Obermaier B.,
 RA Fartmann B., Valie G., Grivelle L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Delseny M., Boutry M., Grivelle L.A., Mache R., Puigdomenech P.,
 RA Wurmbach E., Draneck H., Erffle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Palavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsieck G.,
 RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottewaelde B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Goret P., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.-X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shear T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S.,
 RA Pai G., Millscheer J., Seilers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Saizberg S.L., White O., Venter J.C.,
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 RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanebe A., Yamada M., Yasuda M., Tabata S.,
 RA RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
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 RL Nature 408:820-822(2000).
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 RA Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,
 RA Becker J.;
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 CC -I- SUBUNITS: HOMODIMER (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -I- PTM: THE CYS-119-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 H2O2(O2), AND THE OXIDIZED CYS-119 (PROBABLY CYS-SOH) RAPIDLY
 REACTS WITH CYS-241-SH OF THE OTHER SUBUNIT TO FORM AN
 INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

DR InterPro; IPR000866; AhPC-TSA.
 DR Pfam; PR00578; AhPC-TSA; 1.
 RP Antioxidant; Chloroplast; Transit peptide.
 RA KW CHIROPPLAST (BY SIMILARITY).
 RL TRANSIT 1
 FT 65
 CHAIN 66 266
 ACT_SITE 119 2-CYS PEROXIREDOXIN BASI.
 FT 119 BY SIMILARITY.
 FT 241 BY SIMILARITY.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salancikat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Perez-Alonso M., Obermaier B.,
 RA Fartmann B., Valie G., Grivelle L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Delseny M., Boutry M., Grivelle L.A., Mache R., Puigdomenech P.,
 RA Wurmbach E., Draneck H., Erffle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Palavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsieck G.,
 RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottewaelde B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Goret P., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.-X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shear T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S.,
 RA Pai G., Millscheer J., Seilers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Saizberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanebe A., Yamada M., Yasuda M., Tabata S.,
 RA RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
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 RA Becker J.;
 RT "Full length cDNA sequence of Arabidopsis thaliana.";
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 RESPONSE TO A HIGHLY REDUCED CELLULAR THIOL POOL, AND SLIGHTLY
 INDUCED BY OXIDATIVE STRESS.
 CC -I- SUBUNITS: HOMODIMER (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -I- PTM: THE CYS-119-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 H2O2(O2), AND THE OXIDIZED CYS-119 (PROBABLY CYS-SOH) RAPIDLY
 REACTS WITH CYS-241-SH OF THE OTHER SUBUNIT TO FORM AN
 INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB000405; BAA19099_1;
 DR HSSP; P30041; IPRX;
 DR InterPro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 FT ACT-SITE 64 64 BY SIMILARITY.
 FT ACT-SITE 185 185 BY SIMILARITY.
 SQ SEQUENCE 210 AA; 23326 MW; E2D488179D6937E6 CRC64;

Query Match 36.7%; Score 362; DB 1; Length 210;
 Best Local Similarity 38.3%; Pred. No. 1.5e-25; Indels 4; Gaps 2;
 Matches 70; Conservative 37; Mismatches 72; Index 1;
 DR HSSP; P30041; IPRX;
 DR InterPro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.

Qy 1 MSLINNKIKPKFKNQFKNGEEFIEEKDTEGRWSVFFFPADEFVFCPEBLGDYHE 60
 Db 17 LPLVGKNAKDPFAAEVQDFEQFINTVKLSDYIGKKVYLLFVPLDFTFVCPTETAFSDRHE 76
 Qy 61 BLQKLGVDWAVSTDTHTHKAW--HSSSETIATKIKYAMIGDPGALTRNFDDNNREDEG 117
 . :|: ::|: ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 77 EFEKINKTEILGVPSVPSFHAWQPERKSGGLDGKPLVSDVVKSLSKFGVHLKDQ 136
 Qy 118 LADRAFTVFDPOGIIQATEVTAEGICRGDAASDLRKKAQOWASHGEVOPAKWEGEAT 177
 . :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
 Db 137 IALRGFLIDKEGVQHSTINNLIGRSVDETLTRALQV-KAPDEVEPAGWWPGEEKS 195
 Qy 178 LAP 180
 Db 196 MKP 198

RESULT 7

PDX2_RAT ID PDX2_RAT STANDARD; PRT; 198 AA.
 AC P35704;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Peroxiredoxin 2 (thioredoxin peroxidase 1) (thiol-specific antioxidant protein) (TSA).
 PDX2 OR TPX1.
 GN Rattus norvegicus (rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buterilia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId-10116;
 RN [1]
 RP SEQUENCE FROM N A.

PT TISSUE=Brain;
 RX MEDLINE=94316629; PubMed=8041738;
 RA Chae H.Z., Robison K., Poole L.B., Church G., Stoerz G., Rhee S.G.;
 RT "Cloning and sequencing of thiol-specific antioxidant from mammalian brain: alkyl hydroperoxide reductase and thiol-specific antioxidant define a large family of antioxidant enzymes";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10116-1021 (1994).
 CC -----
 - FUNCTION: Reduces peroxides with reducing equivalents provided
 THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE REDUCED ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR CONCENTRATIONS OF H(2)O(2).
 CC -----
 - SUBUNIT: Homodimer; Disulfide-linked, upon oxidation (BY

CC -----
 CC -!- SIMILARITY: SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: THE CYS-51-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY H(2)O(2), AND THE OXIDIZED CYS-51 (PROBABLY CYS-50) RAPIDLY REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -----
 CC -!- SIMILARITY: BELONGS TO THE AHPC-TSA FAMILY.
 CC -----
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 CC -----
 DR DR HSSP; P30041; IPRX;
 DR InterPro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.

Qy 9 KP--FKNQFKNGEEFIEEKDTEGRWSVFFFPADEFVFCPEBLGDYHEELQK 65
 Db 10 KPADPDTGTAVDGFKEIKLSDYGRKG-YVLFYVPLDFTFVCPTETAFSDAHDERFL 68
 Qy 66 GVDVAVSTDTHTHKAWHSSET--IAKIKYAMIGDPGALTRNFDDNNREDEGLADRA 122
 . :|: ::|: ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 69 GCEVLGVPSVDSOFTHLAWINIPRKEGGLGPINIPLLADVVKSLSONGYVILKNDGIAVRG 128
 Qy 123 TVFDVPOGIIATEVTAEGICRGDAASDLRKKAQOWASHGEVOPAKWEGEATLAPS 182
 Db 129 LFIDDKRGVLRQITVNDLPVGRSVDEALRUVQAFQYDTEI-GEVFAGWWPGSDTIKPNV 187
 Qy 183 D 183
 Db 188 D 188

RESULT 8

BASL_HORVU ID BASL_HORVU STANDARD; PRT; 210 AA.
 AC 096468;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 DE PEPTIDE: D-E-A-L-V-I-N-T-E-R-D-E-S-U-L-F-O-D-E-X-O-N
 DE Antioxidant protein (Fragment).

GN BASL
 OS Hordeum vulgare (Barley)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Hordeum.
 RN NCBI_TaxId-4513;
 RP SEQUENCE FROM N A.

RC STRAIN=CV_GERBELL; TISSUE=Leaf;
 RX MEDLINE=95382424; PubMed=8790288;
 RA Bader M., Dietz K.-J.;
 RT "Primary structure and expression of plant homologues of animal and fungal thioredoxin-dependent peroxide reductases and bacterial alkyl hydroperoxide reductases";
 RT Plant Mol. Biol. 31:553-564 (1996).
 CC -----
 -!- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IMPORTANT IN

CC or send an email to license@ib-sib.ch).

RX MDDLINE=93162043; PubMed=1286667;

RA Rasmussen H., van Damme J., Puype M., Geser B., Celis J.E.,

RA Vandekerckhove J.,

RT "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes.";

RT Electrophoresis 13:960-965(1992).

RN [5]

RN SEQUENCE OF 17-26 AND 93-103.

RC TISUB-Erythrocyte;

RX MEDLINE=94147970; PubMed=8313871;

RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A., Walzer C.,

RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Ballant L., Hochstrasser D.F.,

RT "Plasma and red blood cell protein maps: update 1993.";

RL Electrophoresis 14:1223-1231(1993).

[6]

RN SEQUENCE OF 17-26; 111-135 AND 140-157.

RP TISSUE=Colon carcinoma;

RX MEDLINE=91295306; PubMed=9150948;

RA JI, H., Reid G.E., Moritz R.L., Eedes J.S., Burgess A.W., Simpson R.J.,

RT "A two-dimensional gel database of human colon carcinoma proteins.";

RL Electrophoresis 18:605-613(1997).

CC - FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR NECROSIS FACTOR ALPHA BY REGULATING THE INTRACELLULAR CONCENTRATIONS OF H₂O₂.

CC - FUNCTION: ENHANCES NATURAL KILLER (NK) CELLS ACTIVITY BY REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE REDUCED BY THIOREDOXIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE AhPC-TSA FAMILY.

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CC

RX MEDLINE=94193012; PubMed=8144038;

RA Lim Y.-S., Cha M.-K., Kim H.-K., Kim I.-H.;

RT "The thiol-specific antioxidant protein from human brain: gene cloning and analysis of conserved cysteine regions.";

RT Gene 140:279-284(1994).

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=9429283; PubMed=8026862;

RA Shau H., Butterfield L.H., Chiu R., Kim A.;

RT "Cloning and sequence analysis of candidate human natural killer-enhancing factor genes.";

RT Immunogenetics 40:128-134(1994).

RN [3]

RN SEQUENCE OF 35-198 FROM N.A.

RA Oberbaumer I.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

RN [4]

RN SEQUENCE OF 17-25; 140-150 AND 163-185.

RC TISSUE=Keratinocytes;

Query Match 35-198; Score 346.5; DB 1; Length 198;

Best Local Similarity 38.7%; Pred. No. 6.3e-24;

Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

QY	5	NRKIKD--FKNQAFKNGEETILEKEOTEGRMSVFVFFYPADTFVCPTELGVDADHYE 60
Db	5	NARIGKAPPDKATAVVYDGAKFVKLSDYKGKY-VVLFYPLDFVCPTEITAFSNRAE 63
QY	61	EOKLGLDVYAVSTDTHFTKWAHSSET--IAKIVYAMGDPGALTNRNFNDMREDE 117
Db	64	DPRKLGSCEVLGVSVSDQFTHLWINTPKKEGGLGPLNPLADVTRRISEDYQVLTDEC 123
QY	118	LADRATFVDPQGIQIAQIETVTAEGIGRDAASDLRLRKIAAQYVASHPGEVCPAKWKEGAT 177
Db	124	IAYRGLFDIDKGVLQRQITVNDLPVGRSVDEALRLVQAFQYTDHE-GEVCPAGWPGSDT 182
QY	178	LAPSLD 183
Db	183	IKPNVD 188
RESULT 13		
PDX1_RAT	STANDARD;	PRT; 199 AA.
PDX1_RAT	ID: 063716;	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	peroxiredoxin 1 (thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Heme-binding 23 kDa protein) (HBP23).	
GN	PRDX1 OR TPX2.	
OS	Rattus norvegicus (Rat).	
OC	Bukarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
OX	NCBI_TaxId=10116;	
RN	[1] SEQUENCE FROM N.A.	
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=liver;	
RX	MEDLINE=96072454; PubMed=577926;	
RA	Iwahara S.-I., Satoh H., Song D.-X., Webb J., Burlingame A.L., Nagae Y., Muller-Eberhard U., Purification, characterization, and cloning of a heme-binding protein (23 kDa) in rat liver cytosol. <i>Biochemistry</i> 34:13398-13406(1995).	
CC	-!- FUNCTION: Reduces peroxides with reducing equivalents provided through the thioredoxin system. It is not able to receive electrons from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2).	
CC	-!- SUBUNIT: Homodimer. Disulfide-linked, upon oxidation (by similarity), may form heterodimers with the antioxidant protein 2.	
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.	
CC	-!- PTM: The CYS-52-SH group is the primary site of oxidation by H(2)O(2), and the oxidized CYS-52 (probably CYS-SOH) rapidly reacts with CYS-173-SH of the other subunit to form an intermolecular disulfide. This disulfide might subsequently be reduced by thioredoxin (by similarity).	
CC	-!- SIMILARITY: Belongs to the AHC/TS4 family.	
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CC	EMBL; D30035; BAA06275_1.	
CC	DR Pfam PF00578; Ahpc-TSA; 1.	
KW	Antioxidant.	
FT	ACT SITE 52 BY SIMILARITY.	
ACT SITE 173 BY SIMILARITY.		
FT	SEQUENCE 199 AA; 22109 MW; BDFFD4ABABA775DA CRC64;	
CC	DR	
RESULT 14		
PDX3_MOUSE	STANDARD;	PRT; 257 AA.
PDX3_MOUSE	ID: P20108;	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)	
DT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	Thioredoxin-dependent peroxide reductase, mitochondrial precursor (Perioredoxin 3) (Antioxidant protein 1) (AOP-1) (MERS protein) (PRX III).	
DE	PRDX3 OR AOP1 OR MERS.	
GN	OC	
OS	OC	
RN	OC	
RP	OC	
RP	OX	
RP	NCBI_TaxId=10090;	
RP	[1] SEQUENCE FROM N.A.	
RP	MEDLINE=90060782; PubMed=2583515;	
RA	Yamamoto T., Natori S., Obinata M.; "Cloning of a housekeeping-type gene (MRS5) preferentially expressed in murine erythroleukemia cells. "	
RT	Genes 80:337-343 (1999).	
RL	CC	
CC	-!- FUNCTION: Thioredoxin-dependent peroxide reductase. Protects radical-sensitive enzymes from oxidative damage by a radical-generating system (by similarity).	
CC	-!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (by similarity).	
CC	-!- SUBCELLULAR LOCATION: Mitochondrial (Potential).	
CC	-!- TISSUE SPECIFICITY: Housekeeping-type gene preferentially expressed in murine erythroleukemia (MEL) cells.	
CC	-!- INDUCTION: Expression is increased after induction of MEL cells to differentiation by dMSO.	
CC	-!- PTM: The CYS-109-SH group is the primary site of oxidation by H(2)O(2), and the oxidized CYS-109 (probably CYS-SOH) rapidly reacts with CYS-230-SH of the other subunit to form an intermolecular disulfide. This disulfide might subsequently be reduced by thioredoxin (by similarity).	
CC	-!- SIMILARITY: Belongs to the AHC/TS4 family.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	DR	
EMBL; M28723; AAA39524_1.	DR	
PIR; JQ0064; JQ0064.	DR	
HSRP; P30041; IPRX.	DR	

Mon May 20 10:35:10 2002

us-09-679-705-24.rsp

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GenCore version 4.5

On protein - protein search, using sw model

Run on: May 19, 2002, 00:37:01 ; Search time 97.3 Seconds
(without alignments)

Scoring table: 334.255 Million cell updates/sec

Title: US-09-679-705-24

Perfect score: 987

Sequence: 1 MSINTKIKPFKNQAFKNGE.....AKWKEGEATLAPSLLDVGKI 188

Searched: 562222 seqs, 172994929 residues

Total number of hits satistyfing chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTMBML.19:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_orphanelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacterioplasm:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	742.5	75.2	187	16	Q9A4B8	09a4b8 caulobacter
2	719.5	72.9	187	2	082863	082863 pseudomonas
3	714	72.3	206	16	09Pd49	09pd49 xylella fas
4	687.5	69.7	187	2	Q9H10	Q9h10 thermus aqu
5	662	67.1	188	2	087200	087200 amphicill
6	64.5	65.3	189	16	053647	053647 staphylococ
7	631.5	64.0	188	2	Q9R072	Q9r072 bacteroides
8	629	63.7	186	16	Q99XK7	Q99xk7 streptococc
9	626	63.4	186	2	06265	06265 streptococc
10	605.5	61.3	187	16	Q9I6Z3	Q9i6z3 pseudomonas
11	603.5	61.1	187	16	Q9CIL9	Q9cil9 lactococcus
12	589.5	59.7	187	2	006464	006464 xanthomonas
13	563.5	57.1	187	2	030738	030738 enterococcus
14	488.5	49.5	188	16	083522	083522 treponema p
15	455.5	46.1	211	16	066779	066779 aquifex aeo
16	385	39.0	174	17	Q97C80	Q97c80 thermoplas

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	187 AA.
ID Q9A4B8				
AC Q9A4B8;				
DT 01-JUN-2001 (TREMBL: 17, Created)				
DT 01-JUN-2001 (TREMBL: 17, Last sequence update)				
DT 01-DEC-2001 (TREMBL: 19, Last annotation update)				
DE ALKYL HYDROPEROXIDE REDUCTASE, SUBUNIT C.				
GN C22918.				
OS Caulobacter crescentus.				
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;				
CAULOBACTER				
NCBI TAXID=69394;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=ATCC 19089 / CB15;				
RD MEDLINE=2117698; PubMed=1259647;				
RA Neiman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,				
RA Eisen J., Heidelberg J.F., Alley M.R.K., Onia N., Maddock J.R., Ely B.,				
RA Potocka I., Nelson W.C., Newton A., Stephen C., Phadke N.D., Debay R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,				
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J.J., Berry K., Utterback R., Tran K., Wolf A., Yamathavan J., Embley M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,				
RA "Complete genome sequence of Caulobacter crescentus."; Prok Natl Acad Sci U.S.A. 98:4136-4141(2001); EMBL: AE00596; AAC24880.1; -.				
DR TIGR: CC2918; -.				
DR InterPro: IPR00866; APC-TSA.				
DR Pfam: PF00578; APC-TSA; 1.				
KW Complete proteome.				
SQ SEQUENCE 187 AA; 2027 MW: 3079FAB56293CD37 CRC64;				
Query Match 75.2%; Score 742.5; DB 16; Length 187;				
Best Local Similarity 72.3%; Pred. No. 5.4e-61; Mismatches 27; Indels 1; Gaps 1;				
Matches 136; Conservative 27; Mismatches 24; Indels 1; Gaps 1;				
QY 1 MSINTKIKPFKNQAFKNGEFITEKTEGRNSVFFPYADFTFVCPTELGDVADIVE 60				

Db	1	MSLINTKPKPKNAQKFEEFIEFTEDEGKRSVFFFYPADEFTFCPTEGDVAHYE 60	GN	XE1530.
OY	61	ELQKLGVYAVSTDTHTHKAWHSSETTAKIKYAMGDPGALTRNFDRNREDEGLAD 120	OS	Xylella fastidiosa.
Db	60	ERQKLGVYAVSTDTHTHKAWHSSETTAKIKYAMGDPGALTRNFDRNREDEGLAD 119	OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OY	121	RATFVVDPGQIQAIEVTAEGGRDASDLRKTKAAQYVASHRGPEVCAPKWKEGEATLAP 180	OC	Xylella.
Db	120	RGTFLVDPQGVIFMVEVTAEGIGRNAILRKKAQYVAHPGEVCAPKWBEGETLAP 179	OX	Xylella; <i>Nectrioides</i> ; <i>Nectrioides</i> sp.; <i>Nectrioides</i> sp.
OY	181	SLDVVKI 188	OX	Xylella fastidiosa.
Db	180	SLDVVKI 187	OX	Xylella fastidiosa.
RESULT	2		SEQUENCE FROM N.A.	
ID	082863	PRELIMINARY;	PRT;	187 AA.
AC	082863;	01-NOV-1998 (TREMBrel. 08, Last sequence update)	STRAIN=9A5C;	
DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)	LINE-20365717; PubMed=10910347;	MATERIAL;	
DE	AHPC.	SIMPSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Encencio M., Barros M.H., Bonacorso E.D., Bordim S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C.I., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristoffani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Frota J.S., Franca S.C., Franco M.C., Froime M., Furian L.R., Garnier M., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Honeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kurama E.E., Laioret F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeir A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.B.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracco E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nanni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Oliveira M.C., de Oliveira M.C., de Oliveira R.C., Palmeiro D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Savasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchako M.H., Vailada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zattz M., Meléndez J., Setubal J.C.; "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> ."; Nature 406:151-159 (2000).	ORGANISM;	
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	EMBL; AB010689; BA31468.1; -	DR	EMBL; AB003983; AA08439.1; -
DR	HSSP; P30041; IPRX.	DR	HSSP; P30041; IPRX.	
DR	InterPro; IPR000866; Ahpc-TSA.	DR	InterPro; IPR000866; Ahpc-TSA.	
PR	PFam; PF00578; Ahpc-TSA; 1	PR	PFam; PF00578; Ahpc-TSA; 1	
DR	SEQUENCE FROM N.A.	SQ	SEQUENCE FROM N.A.	
OS	Strain=9A5C;	OS	Strain=9A5C;	
OC	"Toluene Induced Constitutive Overexpression of An Alkyl Hydroperoxide Reductase Small Subunit in Pseudomonas putida: Molecular Cloning of the ahp genes.";	OC	"Toluene Induced Constitutive Overexpression of An Alkyl Hydroperoxide Reductase Small Subunit in Pseudomonas putida: Molecular Cloning of the ahp genes.";	
OX	NCBI_TAXID=303;	OX	NCBI_TAXID=303;	
RN	[1]	RN	[1]	
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	
RC	STRAIN=TOL;	RC	STRAIN=TOL;	
RA	Fukumori F., Horikoshi K.; "Toluene Induced Constitutive Overexpression of An Alkyl Hydroperoxide Reductase Small Subunit in Pseudomonas putida: Molecular Cloning of the ahp genes.";	RA	Fukumori F., Horikoshi K.; "Toluene Induced Constitutive Overexpression of An Alkyl Hydroperoxide Reductase Small Subunit in Pseudomonas putida: Molecular Cloning of the ahp genes.";	
RT	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	RT	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	
RT	EMBL; AB010689; BA31468.1; -	RT	EMBL; AB010689; BA31468.1; -	
RT	HSSP; P30041; IPRX.	RT	HSSP; P30041; IPRX.	
PR	InterPro; IPR000866; Ahpc-TSA.	PR	InterPro; IPR000866; Ahpc-TSA.	
DR	SEQUENCE FROM N.A.; 20507 MW; CC6351406B9C8168 CRC64;	SQ	SEQUENCE FROM N.A.; 20507 MW; CC6351406B9C8168 CRC64;	
OS		OS		
OC		OC		
OX		OX		
GN		GN		
Query	Match	72.9%; Score 719.5; DB 2; Length 187;	Query	Match
Best	Local Similarity	67.6%; Pred. No. 7, 3e-59;	Best	Local Similarity
Matches	127; Conservative	134; Mismatches 24; Indels 1; Gaps 1;	Matches	130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
Db	1	MSLINTKPKPKNAQKFEEFIEFTEDEGKRSVFFFYPADEFTFCPTEGDVAHYE 60	Db	1
OY	1	MSLINTKPKPKNAQKFEEFIEFTEDEGKRSVFFFYPADEFTFCPTEGDVAHYE 60	OY	1
Db	1	MSLINTKPKPKNAQKFEEFIEFTEDEGKRSVFFFYPADEFTFCPTEGDVAHYE 60	Db	21
OY	1	MSLINTKPKPKNAQKFEEFIEFTEDEGKRSVFFFYPADEFTFCPTEGDVAHYE 60	OY	1
Db	21	MSVLNTIELLSKATAYKINGQFVSEAVIKWNV-FVYFPADFTFCPTEGDVAHYE 79	Db	21
OY	61	ELQKLGVYAVSTDTHTHKAWHSSETTAKIKYAMGDPGALTRNFDRNREDEGLAD 120	OY	61
Db	60	ERQKLGVYAVSTDTHTHKAWHSSETTAKIKYAMGDPGALTRNFDRNREDEGLAD 119	Db	80
OY	121	RATFVVDPGQIQAIEVTAEGGRDASDLRKTKAAQYVASHRGPEVCAPKWKEGEATLAP 180	OY	121
Db	120	RGTFLVDPQGVIFMVEVTAEGIGRNAILRKKAQYVAHPGEVCAPKWBEGETLAP 179	Db	139
OY	181	SLDVVKI 188	OY	181-SLDVVKI 188
Db	180	SLDVVKI 187	Db	199 SLDVVKI 206
RESULT	3		RESULT	4
ID	09PD49	PRELIMINARY;	PRT;	187 AA.
AC	09PD49;	01-OCT-2000 (TREMBrel. 15, Created)	AC	09K110;
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)	DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)	
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)	DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)	
DE	SUBUNIT C OF ALKYL HYDROPEROXIDE REDUCTASE.	DE	PEROXIREDOXIN.	
GN		GN		
Query	Match	72.3%; Score 714; DB 16; Length 206;	Query	Match
Best	Local Similarity	69.1%; Pred. No. 2.7e-58;	Best	Local Similarity
Matches	130; Conservative	129; Mismatches 27; Indels 2; Gaps 2;	Matches	130; Conservative 27; Mismatches 27; Indels 2; Gaps 2;
Db	1	MSLINTKPKPKNAQKFEEFIEFTEDEGKRSVFFFYPADEFTFCPTEGDVAHYE 60	Db	1
OY	1	MSLINTKPKPKNAQKFEEFIEFTEDEGKRSVFFFYPADEFTFCPTEGDVAHYE 60	OY	1
Db	21	MSVLNTIELLSKATAYKINGQFVSEAVIKWNV-FVYFPADFTFCPTEGDVAHYE 79	Db	21
OY	61	ELQKLGVYAVSTDTHTHKAWHSSETTAKIKYAMGDPGALTRNFDRNREDEGLAD 120	OY	61
Db	80	ERQKLGVYAVSTDTHTHKAWHSSETTAKIKYAMGDPGALTRNFDRNREDEGLAD 119	Db	80
OY	121	RATFVVDPGQIQAIEVTAEGGRDASDLRKTKAAQYVASHRGPEVCAPKWKEGEATLAP 180	OY	121
Db	139	RGTFLVDPQGVIFMVEVTAEGIGRNAILRKKAQYVAHPGEVCAPKWBEGETLAP 198	Db	139
OY	181	SLDVVKI 188	OY	181-SLDVVKI 188
Db	199	SLDVVKI 206	Db	199 SLDVVKI 206

OS	Thermus aquaticus.
OC	Bacteria; Thermus/Deinococcus group; Thermus group: Thermus.
NCBI_TAXID	271;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20459059; PubMed=10862622;
RA	Logan C., Mayhew S.G.;
RT	"Cloning, overexpression, and characterization of peroxiredoxin and
RT	NADH peroxiredoxin reductase from <i>Thermus aquaticus</i> .";
RL	J. Biol. Chem. 275:30019-30028(2000).
DR	EMBL; AF276071; AAF82118.1; -.
SQ	SEQUENCE 187 AA; 20982 MW; F4D33C459D104819 CRC64;
RESULT	5
087200	PRELIMINARY; PRT; 187 AA.
ID	087200
AC	087200;
DT	01-NOV-1998 (TREMBlrel. 08, Created)
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C (EC 1.6.4.-).
GN	AHC; OR SA036 OR SA0581.
OS	Staphylococcus aureus.
OS	Staphylococcus aureus (strain N315), and
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OC	Bacillus/Staphylococcus group; Staphylococcus.
OX	NCBI_TAXID=1280, 158879, 158878;
RN	[1]
RP	SEQUENCE FROM N.A.; STRATN=RNA220;
RC	SPECIES=S.aureus; STRATN=RNA220;
RX	MEDLINE=96004465; PubMed=1551034;
RA	Armstrong-Buisseret L., Cole M.B., Stewart G.S..
RT	"A homologue to the <i>Escherichia coli</i> alkyl hydroperoxide reductase
RT	Ahpc is induced by osmotic upshock in <i>Staphylococcus aureus</i> .";
RL	Microbiology 141:1655-1661(1995).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus; STRAIN=RM4220;
RA	Jones E.C., Francis K.P., Stewart G.S.A.B.;
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX	MEDLINE=21311952; PubMed=11418166;
RA	Kuroda M., Onita T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Liang J.-Q., Ito T.,
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA	Mizutani-Uji T., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA	Sekiizu K., Hirakawa H., Kubara S., Goto T., Yabuzaki J.,
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA	Hataori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT	"Whole genome sequencing of methicillin-resistant <i>Staphylococcus aureus</i> "; Lancet 357:1225-1240(2001).
RL	Lancet 357:1225-1240(2001).
CC	-1- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED DITHIOL FORM (BY SIMILARITY).
CC	-1- INDUCTION: BY OSMOTIC UPSHOCK.
CC	-1- SIMILARITY: BELONGS TO THE AHPC-TSA FAMILY.
DR	EMBL; U92441; AA51151.1; -.
DR	EMBL; AP033130; BAB4153.1; -.
DR	EMBL; AP033139; BAB46543.1; -.
DR	InferPro; IP0000846; AHPC-TSA.1.
DR	Pfam; PF00578; AHPC-TSA.1.
DR	Oxidoreductase; Complete proteome.
SQ	SEQUENCE 189 AA; 20976 MW; B7134A9C84066B73 CRC64;
Query Match	67.1%; Score 662; DB 2; Length 188;
Best Local Similarity	63.0%; Pred. No. 1 6e-53;
Matches	119; Conservative 33; Mismatches 35; Indels 2; Gaps 2;
Qy	1 MSINTKIKPKKQNAFKNG-EFIEITEKDTEGRMSVFFYPAFDFTCVPTELGVDADH 59
Db	1 MSILGIVEVQPFRAQAFQSGKDFEVTEADLGKWSI-VCFYPADFSVCPTLEDOKEY 59
Qy	60 EELQKGIVDVIAVSTDHFTHKIKAWSSETAKIKAMIGDPTGALTRNFNDMREDEGLA 119
Db	60 AEUKKLGVENVISSTDHFVHKAWHENSPAVGSIYINIGDSQTISQFDVINEEGLA 119
Query Match	65.3%; Score 644.5; DB 16; Length 189;
Best Local Similarity	64.2%; Pred. No. 6.6e-52;
Matches	122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;
Qy	1 MSINTKIKPKKQNAFKNG-EFIEITEKDTEGRMSVFFYPAFDFTCVPTELGVDADH 58
Db	1 MSLINKELPFTAQAFDPKKDDKEVTOEDLGKGSWSV-VCFYPADFSVCPTLEDLQHQ 59

QY	59	YEELQKLGIVDVTAVASDTHTRHKAWHSSETIATKIKAMGDPGALTRNFDMRDEG.	Db	Streptococcus
	: : : : : : : : : : : : : : : :	NCBI_TaxID=1314;	OX	
	[1]	RN	SEQUENCE FROM N.A.	
		RP		
		RC	STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;	
		RX	MEDLINE=2192684; PubMed=1129696;	
		RA	Ferretti J.J., McShan W.M., Ajicic D.J., Savic D.J., Savic G., Lyon K.,	
		RA	Primeaux C.J., Sezate S., Savorov A.N., Kenton S., Imai H.S., Lin S.P.,	
		RA	Ojan Y., Jia H.G., Najar B., Ren Q., Zhai H., Song L., White J.,	
		RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;	
		RT	Complete genome sequence of an M1 strain of Streptococcus pyogenes.;"	
		RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).	
		DR	EMBL: AE006228; AAC31732.1; .	
		KW	peroxidase; Complete proteome.	
		SQ	SEQUENCE 186 AA; 20478 MW; 5B7147A476DBAEF1 CRC64;	
RESULT	7			
ID	09RQ72	PRELIMINARY;	PRT; 188 AA.	
ID	09RQ72;			
AC				
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DT	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.			
GN	AHPc			
OS	Bacteroides fragilis.			
OC	Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;			
OC	Bacteroides			
NCBI_TaxID	=817;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=638R;			
RC	MEDLINE=99412269; PubMed=10482511;			
RA	Rocha E.R., Smith C.J.;			
RA	J. Bacteriol. 181:5701-5710(1999).			
RT	"Role of the alkyl hydroperoxide reductase (ahpCF) gene in oxidative stress defense of the obligate anaerobe Bacteroides fragilis."			
RT	J. Bacteriol. 181:5701-5710(1999).			
RL	EMBL: AF129406; AAC52147.1; .			
DR	InterPro: IPR00866; AhpC-TSA.			
DR	Pfam: PF00578; AhpC-TSA; 1.			
SQ	SEQUENCE 188 AA; 21061 MW; 4A474FFF66D6C6614 CRC64;			
Query Match	64.0%	Score 631.5;	DB 2; Length 188;	
Best Local Similarity	60.8%	Pred. No. 1	Le-50;	
Matches	113;	Conservative	28;	
		Mismatches	41;	
		Indels	2;	
		Gaps		
QY	1	MSLINTKIKPKNQAKNGEFEITEKDTEGWSVFFFPADFTVCPTEGDVADHYE	Db	Streptococcus
	: : : : : : : : : : : : : : : :	MSLIGKBAEFSQAQYHDGKFITVTBNDKGW-FCFYPADFESVCPTEBLGQEQYE	Db	Streptococcus
	[1]	59		
QY	61	ELOKLQWAVASTDHTFHTRHKAWHSSETIATKIKAMGDPGALTRNFDMRDEGLAD	Db	Streptococcus
	: : : : : : : : : : : : : : : : :	60 TLKSLQVEVSVYSTDHFVHKAWHDSDSVGTITPMIGDPSHLSSQAFEVTLGER-GLAO	Db	Streptococcus
QY	121	RATFVVDPOGQTIAEVTAEGGRDASDLRKIKAQYVASHPGEVCPAKWKEGEATLAP	Db	Streptococcus
	: : : : : : : : : : : : : : : : :	119 RGTFIVDPOGIIQMIMINADGIRDASTLIDKIHQAQYVRKHMGEVCPAKWKEGEATLIP	Db	Streptococcus
QY	181	SLDWVSKI 188	Db	Streptococcus
QY	179	SLDWVSKI 186	Db	Streptococcus
RESULT	9			
ID	066265	PRELIMINARY;	PRT; 186 AA.	
ID	066265			
AC				
DT	01-AUG-1998 (TREMBLrel. 07, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	ALKYL HYDROPEROXIDASE.			
GN	AHPc			
OS	Streptococcus mutans.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;			
OC	Streptococcus			
NCBI_TaxID	=1309;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCIB 11723;			
RC	MEDLINE=20120050; PubMed=10656297;			
RA	Poolie L., Hijuchi M., Shimada M., Li Calzi M., Kamio Y.;			
RA	"Streptococcus mutans H2O2-forming NADH oxidase is an alkyl hydroperoxide reductase protein.";			
RT	Free Radic. Biol. Med. 28:108-120(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCIB 11723;			
RC	MEDLINE=95036859; PubMed=7765479;			
RA	Higuchi M., Shimada M., Matsumoto J., Yamamoto Y., Rhaman A.,			
RA	Kamio Y.;			
RT	"Molecular cloning and sequence analysis of the gene encoding the H2O2-forming NADH oxidase from Streptococcus mutans."			
RT	Biosci. Biotechnol. Biochem. 58:1603-1607(1994).			
RL	EMBL: AB010712; BAA25695.1; .			
DR	InterPro: IPR00866; AhpC-TSA.			
DR	Pfam: PF00578; AhpC-TSA; 1.			
KW	Peroxidase.			
SQ	SEQUENCE 186 AA; 20478 MW; 1C7E9BEA4D739F06 CRC64;			

	Query Match	63.4%	Score 626; DB 2; Length 186;
Best Local Similarity	60.6%	Pred. No. 3 3e-50;	
Matches	114;	Conservative 29; Mismatches 43; Indels 2; Gaps 2;	
Q	1 MSINTKIKPKFKNQAFKNGEFEITEKDTEGRMSVFFFYADFTFCPTLGVDVADHYE	60	O9CIL9 PRELIMINARY; PRT; 187 AA.
Db	1 MSLVKGVEMVERSAQVHAGFVTVNNDVKVAV-FCFYPADEFSCVCPTELGQEAQY	59	O9CIL9 PRELIMINARY; PRT; 187 AA.
Qy	61 ELQKLGVDVAVASTDTHTKAVHSSETIAKIKYAMGDPGTRNFNMRDEGLAD	120	O9CIL9 PRELIMINARY; PRT; 187 AA.
Db	60 TLQSLGEVVSYSIDTHFVHKAHDSSDVQGTYWMGDSHVLSQGFEELGED-GLAQ	118	O9CIL9 PRELIMINARY; PRT; 187 AA.
Qy	60 TLQSLGEVVSYSIDTHFVHKAHDSSDVQGTYWMGDSHVLSQGFEELGED-GLAQ	118	O9CIL9 PRELIMINARY; PRT; 187 AA.
Db	61 ELQKLGVDVAVASTDTHTKAVHSSETIAKIKYAMGDPGTRNFNMRDEGLAD	120	O9CIL9 PRELIMINARY; PRT; 187 AA.
Qy	121 RAYFWVPPQGIQAIETVAAEGIGRDASDLRKKAQVYASHRGEVCPAKWKEGEATLAP	180	O9CIL9 PRELIMINARY; PRT; 187 AA.
Db	119 RGFTEVDPDGIIOMMEVNADGIGRADSTLIDKVRAQYIROHPGEVCPAKWKEGTLKP	178	O9CIL9 PRELIMINARY; PRT; 187 AA.
Qy	181 SLIDLVGKI 188		O9CIL9 PRELIMINARY; PRT; 187 AA.
b	179 SLIDLVGKI 186		O9CIL9 PRELIMINARY; PRT; 187 AA.
b	179 SLIDLVGKI 186		O9CIL9 PRELIMINARY; PRT; 187 AA.
RESULT	10		
Q	991623 PRELIMINARY; PRT; 187 AA.		
Db	991623 PRELIMINARY; PRT; 187 AA.		
Q	091623; 01-MAR-2001 (TREMBlrel. 16, Created)		
Db	091623; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)		
Q	01-DEC-2001 (TREMBlrel. 19, Last annotation update)		
Db	01-DEC-2001 (TREMBlrel. 19, Last annotation update)		
Q	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.		
Db	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.		
Q	AHPC OR PA0139.		
Db	AHPC OR PA0139.		
Q	091623; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)		
Db	091623; 01-MAR-2001 (TREMBlrel. 16, Last sequence update)		
Q	SEQUENCE FROM N.A.		
Db	SEQUENCE FROM N.A.		
Q	SESTRAIN=ATCC 15992 / PAO1; MEDLINE=20043733; PubMed=0984043;		
Db	SESTRAIN=ATCC 15992 / PAO1; MEDLINE=20043733; PubMed=0984043;		
Q	Stover, C.K., Pham, X.-O.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Gooley, L., Tolentino, E., Westbrook, Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Salter, M.H., Hancock, R.E.W., Lory, S., Olson, M.V.; "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen"; Nature 406:959-964 (2000).		
Db	Stover, C.K., Pham, X.-O.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Gooley, L., Tolentino, E., Westbrook, Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Salter, M.H., Hancock, R.E.W., Lory, S., Olson, M.V.; "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen"; Nature 406:959-964 (2000).		
Q	EMBL: AE004452; AAC03529.1; -.		
Db	EMBL: AE004452; AAC03529.1; -.		
Q	complete proteome; SEQUENCE 187 AA;		
Db	complete proteome; SEQUENCE 187 AA;		
Q	SEQUENCE 187 AA; 20603 MW; BE1454C8FE20DB78 CRC64;		
Db	SEQUENCE 187 AA; 20603 MW; BE1454C8FE20DB78 CRC64;		
RESULT	11		
Q	09CIL9 PRELIMINARY; PRT; 187 AA.		
Db	09CIL9 PRELIMINARY; PRT; 187 AA.		
Q	ID O9CIL9; DT 01-JUN-2001 (TREMBlrel. 17, Created)		
Db	ID O9CIL9; DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)		
Q	AC O9CIL9; DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)		
Db	AC O9CIL9; DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)		
Q	DE ALKYL HYDROPEROXIDE REDUCTASE.		
Db	DE ALKYL HYDROPEROXIDE REDUCTASE.		
Q	GN AHC.		
Db	GN AHC.		
Q	OS Lactococcus lactis (subsp. <i>lactis</i>) (<i>Streptococcus lactis</i>). Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Lactococcus.		
Db	OS Lactococcus lactis (subsp. <i>lactis</i>) (<i>Streptococcus lactis</i>). Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Lactococcus.		
Q	OC Lactococcus.		
Db	OC Lactococcus.		
Q	OX NEBL_TaxID=1360;		
Db	OX NEBL_TaxID=1360;		
Q	RN [1]		
Db	RN [1]		
Q	RP STRAIN=L1403;		
Db	RP STRAIN=L1403;		
Q	RC MEDLINE=2125186; PubMed=11337471;		
Db	RC MEDLINE=2125186; PubMed=11337471;		
Q	RA Botulin A., Wincker P., Manger S., Jallion O., Malarrie K., Weissbach J., Ehrlich S.D., Sorkin A.; "The complete genome sequence of the lactic acid bacterium <i>Lactococcus lactis</i> ssp. <i>lactis</i> IL1403." Genome Res. 11:731-753 (2001).		
Db	RA Botulin A., Wincker P., Manger S., Jallion O., Malarrie K., Weissbach J., Ehrlich S.D., Sorkin A.; "The complete genome sequence of the lactic acid bacterium <i>Lactococcus lactis</i> ssp. <i>lactis</i> IL1403." Genome Res. 11:731-753 (2001).		
Q	DR InterPro: IPR000866; AHPc-TSA; 1.		
Db	DR InterPro: IPR000866; AHPc-TSA; 1.		
Q	DR Pfam: PF00578; AHPc-TSA; 1.		
Db	DR Pfam: PF00578; AHPc-TSA; 1.		
Q	KW Complete proteome; DR InterPro: IPR000866; AHPc-TSA; 1.		
Db	KW Complete proteome; DR InterPro: IPR000866; AHPc-TSA; 1.		
Q	SQ SEQUENCE 187 AA; 20603 MW; BE1454C8FE20DB78 CRC64;		
Db	SQ SEQUENCE 187 AA; 20603 MW; BE1454C8FE20DB78 CRC64;		
RESULT	12		
Q	Query Match	61.1%	Score 603.5; DB 16; Length 187;
Best Local Similarity	58.5%	Pred. No. 4.1e-48;	
Matches	110;	Conservative 33; Mismatches 44; Indels 1; Gaps 1;	
Q	1 MSINTKIKPKFKNQAFFNGEFEITEKDTEGRMSVFFFYADFTFCPTLGVDVADHYE	60	O9CIL9 PRELIMINARY; PRT; 187 AA.
Db	1 MSLVKGKIEEFTDAYLGKFTKVSDFKDFGKSYDFVCPTELGQEAQY	59	O9CIL9 PRELIMINARY; PRT; 187 AA.
Q	61 ELQKLGVDVAVASTDTHTKAVHSSETIAKIKYAMGDPGTRNFNMRDEGLAD	120	O9CIL9 PRELIMINARY; PRT; 187 AA.
Db	60 TLQSLGEVVSYSIDTHFVHKAHDSSDVQGTYWMGDSHVLSQGFEELGED-GLAQ	119	O9CIL9 PRELIMINARY; PRT; 187 AA.
Q	121 RAYFWVPPQGIQAIETVAAEGIGRDASDLRKKAQVYASHRGEVCPAKWKEGEATLAP	180	O9CIL9 PRELIMINARY; PRT; 187 AA.
Db	120 RGFTEVDPDGIIOMMEVNADGIGRADSTLIDKVRAQYIROHPGEVCPAKWKEGTLKP	179	O9CIL9 PRELIMINARY; PRT; 187 AA.
Q	181 SLIDLVGKI 188		
b	180 SLIDLVGKI 187		
RESULT	12		
Q	006464 PRELIMINARY; PRT; 187 AA.		
Db	006464 PRELIMINARY; PRT; 187 AA.		
Q	ID 006464; DT 01-JUL-1997 (TREMBlrel. 04, Created)		
Db	ID 006464; DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)		
Q	AC 006464; DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)		
Db	AC 006464; DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)		
Q	DE ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.		
Db	DE ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.		
Q	GN AHC.		
Db	GN AHC.		
Q	OS Xanthomonas campestris (pv. <i>phaseoli</i>). Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xanthomonas.		
Db	OS Xanthomonas campestris (pv. <i>phaseoli</i>). Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xanthomonas.		
Q	OC NCBL_TAXID=59445;		
Db	OC NCBL_TAXID=59445;		
Q	RN SEQUENCE FROM N.A.		
Db	RN SEQUENCE FROM N.A.		
Q	RP STRAIN=PHAS011;		
Db	RP STRAIN=PHAS011;		
Q	RC MEDLINE=9733113; PubMed=9190810;		
Db	RC MEDLINE=9733113; PubMed=9190810;		
Q	RX RA Loprasert S., Atcharapongkul S., Whangsuk W., Mongkolsuk S.; "Isolation and analysis of the xanthomonas Alkyl hydroperoxide reductase gene and the peroxide sensor regulator genes ahpC and ahpR-oxr-OrfX." 179		
Db	RX RA Loprasert S., Atcharapongkul S., Whangsuk W., Mongkolsuk S.; "Isolation and analysis of the xanthomonas Alkyl hydroperoxide reductase gene and the peroxide sensor regulator genes ahpC and ahpR-oxr-OrfX." 179		
Q	RN 180 SLIDLVGKI 187		
Db	RN 180 SLIDLVGKI 187		

RL	J. Bacteriol. 179:3944-3949(1997).
DR	EMBL; U94336; AAC45425.1; -.
DR	InterPro; IPR000866; Ahpc-TSA.
DR	Pfam; PF00578; Ahpc-TSA; 1.
SQ	SEQUENCE 187 AA; -20462 MW; 844A5ABC4EGAC4 CRC64;
RESULT	14
Query Match	59.7%; Score 589.5; DB 2; Length 187;
Best Local Similarity	56.9%; Pred. No. 8.1e-47;
Matches	107; Conservative 33; Mismatches 47; Indels 1; Gaps 1;
QY	1 MSLINTKIRPKFKNQAFKNGEETIEPKDTEGRWSVFFYPAFDTFVCPTELGVDADYE 60
Db	1 MSLINTKIRPKFKNQAFKNGEETIEPKDTEGRWSVFFYPAFDTFVCPTELGVDADYE 60
QY	61 ELQKLGVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTTRNFNDMREDEGLAD 120
Db	60 ELQKLGVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTTRNFNDMREDEGLAD 120
QY	60 AFKAGAEYIVTIDTHFSHKVNRNETSPAVGKQPLGDPTKLRTRAFGVHTEEGIAL 119
Db	60 AFKAGAEYIVTIDTHFSHKVNRNETSPAVGKQPLGDPTKLRTRAFGVHTEEGIAL 119
SY	121 RATFVWDPGQIQAIEVTAEGIGRDAASDLRKTKAAQYHNGNFIETEASLKGKWSLIFM-PAAFTFNCPETEVEDAADNYA 59
Db	180 SLDLVGKI 187
QY	181 SLDLVGKI 188
Db	180 SLDLVGKI 187
RESULT	13
ID	030738 PRELIMINARY; PRT; 187 AA.
AC	030738; -
DT	01-JAN-1998 (TREMBlrel. 05, Created)
DT	01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE	ALKYL HYDROPEROXIDE REDUCTASE (AHPC).
OS	Treponema pallidum.
OC	Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX	NCBI_TaxID=160;
RP	[1]
RC	SEQUENCE FROM N.A.
STRAIN=NICHOOLS;	
RA	MEDLINE=9833770; PubMed=9655876;
RA	Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwynn M., Hickie E.K., Clayton R., Ketchum K.A., Soifergren E., Harcham J.M., McLeod M.P., Salzberg S., Peterson J.T., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S., Harsh B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
RA	"Complete genome sequence of treponema pallidum, the syphilis spirochete,"
RT	Science 281:375-388(1998);
RL	EMBL; AEG0122; AAC65497.1; -.
DR	HSSP; P3041; 1PRX.
DR	TIGR; TP0509; -
DR	InterPro; IPR000866; Ahpc-TSA.
DR	Pfam; PF00578; Ahpc-TSA; 1.
KW	Complete proteome.
SQ	SEQUENCE 188 AA; 20709 MW; 44D2CFDA3420AFE CRC64;
RESULT	14
Query Match	49.5%; Score 488.5; DB 16; Length 188;
Best Local Similarity	49.7%; Pred. No. 1.8e-37;
Matches	93; Conservative 32; Mismatches 61; Indels 1; Gaps 1;
QY	2 SLINTKIRPKFKNQAFKNGEETIEPKDTEGRWSVFFYPAFDTFVCPTELGVDADYE 61
Db	3 SLIGKRVIFDKLPAYVGKFTEVSNASIKGSWAV-FMFYPAFDTFVCPTELGVDADYE 61
QY	62 LQKLGVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTTRNFNDMREDEGLAD 121
Db	62 FVEIGCKVSVSTDSEYVHKWADATDTKILPYEMITSDKAGKLAGFFGVILLPDWHALR 121
QY	122 ATFWVWDPGQIQAIEVTAEGIGRDAASDLRKTKAAQYHNGNFIETEASLKGKWSLIFM-PAAFTFNCPETEVEDAADNYA 59
Db	122 GTFVWVDPGQIQAIEVTAEGIGRDAASDLRKTKAAQYHNGNFIETEASLKGKWSLIFM-PAAFTFNCPETEVEDAADNYA 59
QY	182 LLDLVGKI 188
Db	182 IDLVGKI 188
RESULT	15
ID	066779 PRELIMINARY; PRT; 211 AA.
AC	066779; -
DT	01-AUG-1998 (TREMBlrel. 07, Created)
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT	01-AUG-2001 (TREMBlrel. 17, Last annotation update)
DE	ALKYL HYDROPEROXIDE REDUCTASE.
GN	AHPC OR AQ_486.
OS	Aquifex aeolicus.
OC	Bacteria; Aquificales; Aquificaceae; Aquifex.
OX	NCBI_TaxID=63363;

Query Match 57.1%; Score 563.5; DB 2; Length 187;
 Best Local Similarity 54.3%; Pred. No. 2.1e-44;
 Matches 102; Conservative 39; Mismatches 46; Indels 1; Gaps 1;

QY 1 MSLINTKIRPKFKNQAFKNGEETIEPKDTEGRWSVFFYPAFDTFVCPTELGVDADYE 60
 Db 1 MNLINQKLFDFECDAVHDGEETRVSFEDLQKGWSI-FFFYPAFDSFCVCPPEBLGDMQEHYA 59

QY 61 ELQKLGVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTTRNFNDMREDEGLAD 120
 Db 60 HLQELNCVEVSYSEDHVHRAWADATEIGKIKPMLADENGQJLARFFGVLDEASGMAY 119

QY 121 RATFVWDPGQIQAIEVTAEGIGRDAASDLRKTKAAQYHNGNFIETEASLKGKWSLIFM-PAAFTFNCPETEVEDAADNYA 59
 Db 120 RASFIVSPEGDIKSYEINDMGIGRNAAEELVKLEASOFVAEHGDKVCPAWQPEETIAP 179

Search completed: May 19, 2002, 03:42:18
Job time: 11117 sec

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